

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 12:35:36 ; Search time 2278.89 Seconds  
(without alignments)  
4026.354 Million cell updates/sec

Title: US-10-622-407-7  
Perfect score: 1550  
Sequence: 1 ttgcactggccatgttgg.....aatgcaaaaaaaaaaaaaa 1550

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1550	100.0	1550	10	Aad64754
2	1550	100.0	1550	12	Adj45751 Murine tm
3	1182.4	76.3	1509	2	Aav68046 Nucleic a
4	1182.4	76.3	1509	12	Adm46622 Mouse 7P4
5	709.4	45.8	967	12	Adf57550 Mouse ymk
6	602	38.8	702	10	Aad64755 Mouse tms
7	602	38.8	702	12	Adj45753 Murine tm
8	514.6	33.2	1200	10	Aad64758 Mouse tms
9	514.6	33.2	1200	12	Adj45757 Murine tm
10	465.4	30.0	503	10	Adj45752 Murine mit
11	432.2	27.9	603	10	Adj45753 Mouse mit
12	412	26.6	412	10	Aad64753 Mouse tms
13	412	26.6	412	12	Adj45749 Murine tm
14	392	25.3	415	6	Abs69674 Novel mur
15	253.2	16.3	357	12	Adf57563 Mouse ymk
16	221.8	14.3	1197	5	Aas73531 DNA encod
17	217	14.0	38920	12	Adg97252 Mouse can
18	205.6	13.3	124289	11	Acn44392 Mouse gen
19	191.6	12.4	203070	11	Acn44012 Mouse gen
20	187.6	12.1	110000	13	ABD32909_1

21	187	12.1	111836	13	ABD33102	Abd33102 Murine ca
22	182.2	11.8	35425	12	ADQ59455	Adq59455 Human can
23	178.2	11.5	71057	11	ACN44120	Acn44120 Mouse gen
24	168.6	10.9	56587	11	ACN44972	Acn44972 Mouse gen
25	167.4	10.8	27299	11	ACN44472	Acn44472 Mouse gen
26	166.4	10.7	134442	13	ABD32824	Abd32824 Mouse can
27	166.2	10.7	121129	13	ABD33446	Abd33446 Murine ca
28	164	10.6	203070	11	ACN44012	Acn44012 Mouse gen
29	161.4	10.4	150351	13	ABD33360	Abd33360 Murine ca
30	160.8	10.4	151858	13	ABD33489	Abd33489 Murine ca
31	160.6	10.4	254481	12	ADQ97135	Adq97135 Mouse can
32	159.6	10.3	51281	9	ADA02873	Ada02873 Mouse Dpt
33	159.6	10.3	51281	10	ABD72611	Abd72611 Mouse Dct
34	159.6	10.3	51281	10	ADC85352	Adc85352 Human Sel
35	159.6	10.3	51281	12	ADM74468	Adm74468 Murine ca
36	159.6	10.3	159434	12	ADQ97730	Adq97730 Mouse can
37	156	10.1	175603	12	ADQ97554	Adq97554 Mouse can
38	154.8	10.0	59158	8	ABX16390_6	Abx16390_6 Continuation (7 of
39	154.8	10.0	110000	8	ABX16390_5	Abx16390_5 Continuation (6 of
40	154.8	10.0	117382	11	ACN44804	Acn44804 Mouse gen
41	154.2	9.9	110000	13	ABD32909_4	Abd32909_4 Continuation (5 of
42	154	9.9	89756	13	ABD32890	Abd32890 Mouse can
43	153.6	9.9	122859	11	ACN43872	Acn43872 Mouse can
44	151.2	9.8	228006	12	ADQ97143	Adq97143 Mouse gen
45	150.6	9.7	185555	11	ACN45180	Acn45180 Mouse gen

ALIGNMENTS

RESULT 1  
AAD64754  
ID AAD64754 standard; cDNA; 1550 BP.  
XX  
AC AAD64754;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Mouse tmst2-receptor cDNA.  
XX  
KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;  
KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;  
KW cancer; chromosome identification; gene therapy; antibacterial; virucide;  
KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;  
KW cytostatic; mouse; gene; ss.  
XX  
OS Mus musculus.  
FH Key Location/Qualifiers  
CDS 13..609  
FT /\*tag= a  
FT /product= "Mouse tmst2 receptor protein"  
XX  
PN US6627199-B1.  
XX  
PD 30-SEP-2003.  
XX  
PP 07-JUL-2000; 2000US-00612033.  
XX  
PR 09-JUL-1999; 99US-0143063P.  
XX  
PA (AMGE-) AMGEN INC.  
XX  
PI Saris C;  
XX  
DR WPI; 2003-874309/81.  
DR P-PSDB; ABW02715.  
XX  
PT New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,  
PT treating or ameliorating diseases associated with or resulting from  
PT abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for  
PT chromosome mapping.  
XX









	Qy	1340	CCTCTCCTTTCCCCCCTCTCTTCTGGTGCTTACTTCTCTTCCTCTCCCACTCTCCACGAGC	13399
	Dd	1274	CCTCTCCTTTTCCCCCTCTCTTCTGTGCTCTTAATTTCTCTTCTCTCCCACTCTCCACCAGC	13333
	Qy	1400	CTCCTCTTTAAGGCCCTGAATCAGTCTGTAGGTGCATGTTTTAAATCTACTACTTTTCTCTCTGCT	1459
	Dd	1334	CGCCTCTTAAGGCCCTGAGTCAGTCTGAGGCCATGTTTAATCTACTACTTTTCTCTCTGCT	1393
	Qy	1460	CTGGACTCATCCAGATGCTCTCTGGCTGAGCTCTCCCTCTATCTACAATAAAAACCCCTTC	1519
	Dd	1394	CTGGACTCATCCAGATGCTCTCTGGCTGAGCTCTCCCTCTATCTACAATAAAA-CCITCC	1452
	Qy	1520	CCCTAACCAAGAATGCAAAA	1539
	Dd	1453	CCCTAACCAAGAATGGAACA	1472
	 RESULT 4 ADM46622 ADM46622 standard; DNA; 1509 BP.			
	XX	AC	ADW46622;	
	XX	AC		
	DT	17-JUN-2004	(first entry)	
	XX		Mouse 7F4 encoding sequence.	
	XX			
	KW	7F4 gene; Osteopathic; Anorectic; Antidiabetic;		
	KW	glycolipid metabolism disorder; osteoporosis; obesity; diabetes; ds.		
	XX	Mus musculus.		
	OS			
	XX			
	FH	Key	Location/Qualifiers	
	FT	CDS	12..542	
	FT		/*tag= a	
	FT		/product= "7F4"	
	XX			
	PN	WO2004026026-A1.		
	XX			
	PD	01-APR-2004.		
	XX			
	Pf	10-SEP-2003; 2003WO-JP011545.		
	XX			
	PR	17-SEP-2002; 2002JP-00270321.		
	XX			
	PA	(CHUS ) CHUGAI SEIYAKU KK.		
	XX			
	PI	Kake T, Saito H, Makishima F;		
	XX			
	DR	WPI; 2004-340227/31.		
	DR	P-PSDB; ADM46623.		
	XX			
	PT	Transgenic non-human animal with modified expression of 7F4 gene for		
	PT	screening remedies for bone or glycolipid metabolism disorders.		
	XX			
	PS	Claim 3; SEQ ID NO 1; 44pp; Japanese.		
	XX			
	CC	The present invention relates to a transgenic non-human animal having the		
	CC	expression of 7F4 gene artificially modified. The transgenic animals are		
	CC	a disease model for bone and glycolipid metabolism disorders. Substances		
	CC	identified by the screening method are agents for the prevention and		
	CC	treatment of diseases including osteoporosis, obesity and diabetes. The		
	CC	present sequence represents the modified mouse 7F4 encoding sequence.		
	XX			
	SQ	Sequence 1509 BP; 387 A; 403 C; 294 G; 425 T; 0 U; 0 Other;		
	 Query Match            76.3%; Score 1182.4; DB 12; Length 1509; Best Local Similarity   90.5%; Pred. No. 1.1e-279; Matches 1321, Conservative   0; Mismatches 101; Indels 38; Gaps 4;			
	Qy	81	GCTGCTCTGCTGCTGCTGAATCTGCCCCTGACGTAAAAATTGCTATGCTAGTAATT	140
	Dd	50	GTTCCTCTTGTCTGCTGCTGCTGAATCTGTTCTTSCCGTAATAATTGCTATGCTGAATC	109



Qy	980	CAGTGCACAACTTCCTCCACAAGGTCATACCTCCTTAATAATACCATTCTTTATGAGGC	1038
Db	906	CAGTGACAAACTTCCTCCACAAGGTCAATACCTCCTTAATAATACCATTCTTTATGAGGC	964
 RESULT 6			
AAD64755	AAD64755 standard; cDNA; 702 BP.		
XX	AC	AAD64755;	
XX	AC		
DT	11-MAR-2004	(first entry)	
XX	DE		
XX	DE	Mouse tmst2-receptor splice variant cDNA.	
XX	KW	Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;	
KW	KW	cachexia; autoimmune disease; inflammatory disease; chromosome mapping;	
KW	KW	cancer; chromosome identification; gene therapy; antibacterial; virucide;	
KW	KW	immunosuppressive; immunomodulator; antinflammatory; antiparasitic;	
KW	KW	cytostatic; mouse; splice variant; gene; ss.	
OS	Mus musculus.		
XX	Key	Location/Qualifiers	
FH	CDS	13..555	
FT	FT	/tag= a	
FT	FT	/product= "Mouse tmst2 receptor splice variant protein"	
XX	US6627199-B1.		
PN			
XX	30-SEP-2003.		
PD			
XX	07-JUL-2000; 2000US-00612033.		
PF			
XX	09-JUL-1999; 99US-0143063P.		
PR			
XX	(AMGE-) AMGEN INC.		
PA			
P1	Saris C;		
XX	WPI; 2003-874309/81.		
DR	P-PSDB; ABW02716.		
XX			
PT	New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,		
PT	treating or ameliorating diseases associated with or resulting from		
PT	abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for		
PT	chromosome mapping.		
XX			
PS	Claim 1; SEQ ID NO 9; Opp; English.		
XX			
CC	The invention relates to transmembrane decoy-receptor (tmst2) proteins		
CC	and their secreted splice variants, belonging to the tumour necrosis		
CC	factor (TNF) receptor super gene family and polynucleotides encoding such		
CC	proteins. The composition and methods are useful in diagnosing, treating		
CC	or ameliorating diseases associated with or resulting from abnormal tmst2		
CC	and/or abnormal expression of its putative ligand, such as sepsis,		
CC	cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial		
CC	and parasitic diseases or cancer. They may also be used for chromosome		
CC	identification or mapping. The invention is useful in gene therapy. The		
CC	present sequence is mouse tmst2-receptor splice variant cDNA used in the		
CC	exemplification of the invention		
XX			
XX	Sequence 702 BP; 163 A; 177 C; 160 G; 202 T; 0 U; 0 Other;		
SQ			
 Query Match                      38.8%; Score 602; DB 10; Length 702;			
Best Local Similarity        93.6%; Pred. No. 2.2e-137;			
Matches 657; Conservative     0; Mismatches    0; Indels    45; Gaps    1			
Qy	1	TTGCATCGGCCCATGTTGGCTTCTTCTTCGACGCTTGCTGTCACGTCGAGTCGCTGCTTC	60
Db	1	TTGCATCGGCCCATGTTGGCTTCTTCTTCGACGCTTGCTGTCACGTCGAGTCGCTGCTTC	60

[illegible]



FH	Key	Location/Qualifiers
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6	6	6
7	7	7
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100	100	100

433 TGCCGCCATGTACCAAGTGTCCTCCCAAGGAATCCCTGCTCCTCAGGAATGCAACTCCACA 492

Db 421 TGCCGCCATGTACCAAGTGCCCAAGGATCCTGTCTCCAGGAATGCAATCTCCACA 480  
Qy 493 GCTAACACTGTGTGAGTTCATCTGTTTCAAAATCCAGAAACCGGCTGTTCTACTGTGA 552  
Db 481 GCTAACACTGTGTGAGTTCATCTGTTTCAAAATGTCGACATCAGATGCCACCGTGC 540  
Qy 553 TCACC 557  
Db 541 CCAGC 545

RESULT 10  
ADD33512/c  
ID ADD33512 standard; DNA; 503 BP.  
AC ADD33512;  
XX  
DT 15-JAN-2004 (first entry)  
DE Mouse mitochondrial DNA sequence SEQ ID NO:1285.  
KW ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;  
KW mitochondrial disease; oxidative phosphorylation dysfunction;  
KW oxidative stress; apoptosis; aging.  
XX  
OS Mus musculus.  
XX  
PN WO2003020220-A2.  
XX  
PD 13-MAR-2003.  
XX  
XX 30-AUG-2002; 2002WO-US027886.  
XX  
XX 30-AUG-2001; 2001US-0316323P.  
PR 31-AUG-2001; 2001CA-02356540.  
XX  
XX (UYEM-) UNIV EMORY.  
PA  
XX Wallace DC, Levy S, Kerstann K, Procaccio V;  
PI WPI; 2003-300821/29.  
DR  
XX Array containing probes for genes involved in mitochondrial biology,  
PT useful for determining mitochondrial biology gene expression profiles for  
PT use in diagnosing pathologies and identifying biochemical pathways.  
XX  
XX Claim 2; SEQ ID NO 1285; 201pp; English.

XX The invention relates to a novel array comprising at least two isolated  
XX nucleotide molecules, each molecule having a sequence capable of uniquely  
XX hybridising to a nucleic acid molecule which is an expression product of  
XX a gene involved in mitochondrial biology. The array comprises two or more  
XX isolated nucleic acid molecules or spots, each molecule having a sequence  
XX chosen from sequence of 994 human probes and 2046 mouse probes. An array  
XX of the invention is useful for determining an expression profile of a  
XX mouse or human sample containing nucleic acid, by contacting the array  
XX with the sample under conditions allowing selective hybridisation, and  
XX measuring hybridisation of nucleic acid in the sample to the array to  
XX produce an expression profile. The array is also useful for determining  
XX an expression profile of a first labelled sample containing nucleic acid  
XX relative to a second, differently labelled sample containing nucleic  
XX acid. The second sample is a reference or a standard. An array is useful  
XX for determining an expression profile diagnostic of an energy-metabolism-  
XX related physiological condition. An array of the invention is useful for  
XX determining mitochondrial biology gene expression profiles of organisms,  
XX such as human, mice and closely related species, tissue and organs of  
XX such organisms, which are useful for determining expression profiles  
XX diagnostic of energy metabolism-related physiological conditions,  
XX diagnosing such physiological conditions, identifying biochemical  
XX pathways, genes, and mutations involved in such physiological conditions,  
XX identifying therapeutic agents useful for preventing and/or treating such  
XX physiological conditions, evaluating and/or monitoring the efficacy of

CC such therapies, and creating and identifying animal models of human  
CC energy metabolism-related physiological conditions. An array is also  
CC useful for defining expression signatures or profiles for mitochondrial  
CC diseases, as well as distinguishing clinical disorders that result from  
CC oxidative phosphorylation (OXPHOS) dysfunction, oxidative stress,  
CC apoptosis and aging. An array of the invention contains probes of genes  
CC not previously recognised to participate in mitochondrial biology. The  
CC sequences shown in ADD33224-ADD35260 represent murine mitochondrial DNA  
CC clones used to make the probes of the invention. Some sequences are not  
CC present, these are SEQ ID NO's 295, 1174, 1213, 1700, 1728, 1730, 1905,  
CC 1906, 2408 and 2643.  
XX

Qy 1025 ATTTCTTATGAGGCAAGCATTCACACATGAGTCTATAGGGGCCAAACCAATTCAAACC 1084  
Db 503 ATTTCTTATGAGGCAAGCATTCACACATGAGTCTATAGGGGCCAAACCAATTCAAACC 444  
Qy 1085 ACCACAGGTTAAACAATTCGCTCTGAGCTCTCTGGTGGAGGCCCTCTTGGAGTAAGT 1144  
Db 443 ACCACAGGTTAAACAATTCGCTCTGAGCTCTCTGGTGGAGGCCCTCTTGGAGTAAGT 384  
Qy 1145 AACAAATTTAGATGAAGGCAAGTCTCTGGTATCAGGTCCAAAGAAACTCAGGATGAATGGT 1204  
Db 383 AACAAATTTAGATGAAGGCAAGTCTCTGGTATCAGGTCCAAAGAAACTCAGGATGAATGGT 324  
Qy 1205 CCAGTGTGGTTCCTATTAAACATGAGTAAGAACATGACCTCACCTTACAGCTCTCCACCTC 1264  
Db 323 CCCTGTGGTTCCTATTAAACATGAGTAAGAACATGACCTCACCTTACAGCTCTCCACCTC 264  
Qy 1265 ACTGACTTCCCTCCCTAGCTTCTCATTCGCCAGGTAACCCCTGCCATTTTGGTAATGT 1324  
Db 263 ACTGGCTTCCCTCCCTAGCTTCTCATTCGCCAGGTAACCCCTGCCATTTTGGTAATGT 204  
Qy 1325 GCCTTCTTGGTTCCTCTCCCTTCTCCCTCTCTTCTGGTCCCTTACTTCTTCTCTCTC 1384  
Db 203 GCCTTCTTGGTTCCTCTCCCTTCTCCCTCTCTTCTGGTCCCTTACTTCTTCTCTCTC 144  
Qy 1385 CCAGTCTCCAGAGCTCTCTTAAAGCCCTGATCAGTCTGATGATCATGTTAAATCTAC 1444  
Db 143 CCAGTCTCCAGAGCTCTCTTAAAGCCCTGATCAGTCTGATGATCATGTTAAATCTAC 86  
Qy 1445 TACTTCTCTCTGCTGAGTCTCATCCAGATGCTCTGGCTGAGCTCTCCCTCTATCTA 1504  
Db 85 TACTTCTCTCTGCTGAGTCTCATCCAGATGCTCTGGCTGAGCTCTCCCTCTATCTA 26  
Qy 1505 CAATAAAACCTTCCCTTAAACAG 1529  
Db 25 CAATAAAACCTTCCCTTAAACAG 1

RESULT 11  
ADD33513  
ID ADD33513 standard; DNA; 603 BP.  
XX  
AC ADD33513;  
XX  
DT 15-JAN-2004 (first entry)  
XX  
DE Mouse mitochondrial DNA sequence SEQ ID NO:1286.  
KW ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;  
KW mitochondrial disease; oxidative phosphorylation dysfunction;  
KW oxidative stress; apoptosis; aging.  
XX  
OS Mus musculus.  
XX  
PN WO2003020220-A2.  
XX







QY 361 TCAGCCACCAGTGACCGGAATGCCAGTCCCGAACAGGCTTTTACTACTATG 412  
DB 361 TCAGCCACCAGTGACCGGAATGCCAGTCCCGAACAGGCTTTTACTACTATG 412

RESULT 14

AB569674  
ID ABS69674 standard; DNA; 415 BP.

AC  
XX  
DT 21-NOV-2002 (first entry)

XX Novel murine polynucleotide isolated using gene trap technology #737.

XX Mouse; gene trapped sequence; GTS; functional genomic analysis;  
KW phase display system; gene chip; temporal gene expression;  
KW tissue specific gene expression; antisense inhibition; gene targeting;  
KW development disorder; cell differentiation disorder; aging; cancer;  
KW autoimmune disease; lupus; inflammatory disorder; skin disorder;  
KW degenerative disorder; ds.

XX Mus musculus.

XX US2002102543-A1.

PN 01-AUG-2002.

XX 30-NOV-2000; 2000US-00728445.

PF 01-DEC-1999; 99US-0168358P.

XX (FRIE/) FRIEDRICH G.

PA (ZAMB/) ZAMBROWICZ B.

PA (SAND/) SANDS A T.

XX Friedrich G, Zambrowicz B, Sands AT;

XX WPI; 2002-690598/74.

XX Novel murine polynucleotides that individually identify novel genes into  
PT which a retroviral gene trap vector has integrated, useful in genomic  
PT analysis and in discovery, development of therapeutic and diagnostic  
PT agents.

PS Claim 1; Page 245; 296pp; English.

XX The invention describes an isolated murine polynucleotide (I) comprising  
CC a contiguous stretch of at least 60 nucleotides of one of 265-677  
CC nucleotide 891 OMIBANK gene trapped sequences (GTSs) (S), given in the  
CC specification. The novel genes and cells are useful in functional genomic  
CC analysis and in the discovery and development of new therapeutic and  
CC diagnostic agents and methods. (I) is useful for identifying the coding  
CC regions of the murine genome, to isolate cDNAs, genomic clones, or full-  
CC length genes/polynucleotides or homologues, heterologues, paralogues, or  
CC orthologues that are capable of hybridising to one or more of the GTSs  
CC under stringent conditions. (I) can be incorporated into a phage display  
CC system that can be used to screen for proteins, or other ligands, that  
CC are capable of binding an amino acid sequence encoded by an  
CC oligonucleotide or polynucleotide sequence in at least one of the TS  
CC sequences. (I) is useful in addressable arrays, such as gene chips, to  
CC identify and characterise temporal and tissue specific gene expression,  
CC to identify the gene of interest from many sources and for genetic  
CC manipulations such as antisense inhibition and gene targeting. Decreasing  
CC the level of expression of (I) and/or down regulating the activity of  
CC peptides or proteins encoded by (I) is useful for treating development  
CC and cell differentiation disorders, aging, cancer, autoimmune disease,  
CC lupus, inflammatory disorders, skin disorders and degenerative disorders.  
CC This sequence represents a murine cDNA isolated using gene trap  
CC technology

XX Sequence 415 BP; 119 A; 107 C; 88 G; 101 T; 0 U; 0 Other;

DR

Query Match 25.3%; Score 392; DB 6; Length 415;  
Best Local Similarity 99.8%; Pred. No. 6.1e-86;  
Matches 403; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 121 AAATTTGCTATGCTAGAAATTACACTCCTTTCAAAATGTCGCGTGGTGAATACTGCTCTAAA 180  
DB 11 AAATTTGCTATGCTAG-ATTACACTCCTTTCAAAATGTCGCGTGGTGAATACTGCTCTAAA 69  
QY 181 GACGCTCTGTTGCAAGAACTGTTCTGAGGTACATTTGTCAAGCGCCCTGCGAAATCCCC 240  
DB 70 GACGCTCTGTTGCAAGAACTGTTCTGAGGTACATTTGTCAAGCGCCCTGCGAAATCCCC 129  
QY 241 CATACTCAAGGACAAATGTCAGAAAGTGTCAAGGAACTTTCACAGAGAAAGATAATTAC 300  
DB 130 CATACTCAAGGACAAATGTCAGAAAGTGTCAAGGAACTTTCACAGAGAAAGATAATTAC 189  
QY 301 CTGGATGCTTGTATATCTTTGCTCCACTGTGATAAAGATCAGGAAATGTCGCGCGACTGC 360  
DB 190 CTGGATGCTTGTATATCTTTGCTCCACTGTGATAAAGATCAGGAAATGTCGCGCGACTGC 249  
QY 361 TCAGCCACCAGTGACCGGAATGCCAGTCCCGAACAGGCTTTTACTACTATGATGACCCAAA 420  
DB 250 TCAGCCACCAGTGACCGGAATGCCAGTCCCGAACAGGCTTTTACTACTATGATGACCCAAA 309  
QY 421 TTTCCAGAAATCGTCGCGCCCATGTACCAAGTGTCCCAAGGATCCCTGTCTCCAGGAA 480  
DB 310 TTTCCAGAAATCGTCGCGCCCATGTACCAAGTGTCCCAAGGATCCCTGTCTCCAGGAA 369  
QY 481 TGCAACTCCACAGCTAAACACTGTGTGCAGTTCATCTGTTTCAA 524  
DB 370 TGCAACTCCACAGCTAAACACTGTGTGCAGTTCATCTGTTTCAA 413

RESULT 15

ADF57563

ID ADF57563 standard; cDNA; 357 BP.

XX ADF57563;

XX 12-FEB-2004 (first entry)

DT Mouse ymkz5 receptor cDNA clone ymkz5-00013-g11.

XX Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour;  
KW cancer; acquired immune deficiency syndrome; AIDS; anaemia;  
KW autoimmune disease; cachexia; leprosy; leukaemia; hepatitis;  
KW multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;  
KW ss; gene.

XX Mus musculus.

OS Key Location/Qualifiers

XX CDS 6..356

XX /tag= a

XX /product= "Murine ymkz5 receptor"

XX /partial

XX /note= "No stop codon"

PN US2003096355-A1.

XX 22-MAY-2003.

XX 11-JUL-2002; 2002US-00193616.

XX 09-JUL-1999; 99US-0143137P.

XX 07-JUL-2000; 2000US-00611989.

XX (ZHAN/) ZHANG K.

XX Zhang K;

XX WPI; 2004-008943/01.

DR P-PSDB; ADF57549.



Result No.	Query			DB	ID	Description
	Score	Match	Length			
C	1	1550	100.0	1550	6	AR403753 Sequence
	2	1537.6	99.2	1555	10	AY046551 Mus muscu
	3	1207	77.9	1491	10	AY165625 Mus muscu
	4	1182.4	76.3	1509	6	AR164284 Sequence
	5	1016	65.5	203141	10	AC068006 Mus muscu
	6	1016	65.5	281000	10	MMU276505 Mus muscu
	7	673	43.4	691	10	AY165627 Mus muscu
C	8	618	39.9	736	10	AY165626 Mus muscu
	9	602	38.8	702	6	AR403754 Sequence
	10	514.6	33.2	1200	6	AR403757 Sequence
	11	494.6	31.9	669	10	MMU278265 Mus muscu
	12	435.8	28.1	240262	2	AC129151 Rattus no
	13	412	26.6	412	6	AR403752 Sequence .
	14	407.8	26.3	569	10	MMU278264 Mus muscu
C	15	402.2	25.9	531	10	AY046550 Mus muscu
	16	232	15.0	217774	2	AC120603 Rattus no
	17	232	15.0	232893	2	AC096182 Rattus no
	18	232	15.0	286640	2	AC127881 Rattus no
	19	231.4	14.9	131919	10	AC096622 Mus muscu
	20	231.4	14.9	131919	10	AC096622 Mus muscu
	21	231.4	14.9	131919	10	AC096622 Mus muscu











DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fato, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nguyen, T., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Piere, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (01-APR-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 On Feb 5, 2004 this sequence version replaced gi:41315175.  
 All repeats were identified using RepeatMasker:  
 Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>  
 ----- Genome Center  
 Center: Whitehead Institute/MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@broad.mit.edu](mailto:sequence_submissions@broad.mit.edu)  
 ----- Project Information  
 Center project name: L5724  
 Center clone name: 6\_I\_17  
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Some of the sequence contained within base pairs 1 - 31513 was  
 stolen from accession AC023248.

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		/clone_lib="RPCI-23 Female Mouse BAC"
misc_feature	1. .6750	/note="wgs end extension"
		clone_end:SP6"
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repeat_region	2370. .2508	/rpt_family="B1_MM"
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repeat_region	2824. .2873	/rpt_family="(CA)n"
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repeat_region	5411. .5445	/rpt_family="(GGA)n"
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repeat_region	14817. .14962	
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Query Match	Score	DB	Length
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Matches 1028;	Conservative	0; Mismatches 20; Indels	0; Gaps 0;

  

Qy	492	AGCTAACACGTGTGTCAGTTTCATCTGTTTCAATCCAGAAACCGGTGTTCTTACTGTT	551
Db	144233	ACCAAAATGTTTCTGTTTTCACACITTTAGATCCAGAAACCGGTGTTCTTACTGTT	144174
Qy	552	ATCACCTTTGAGTGTGCTAATTTGTCGGTTGTTGTTTCCGTATCATAGAATAAAG	611
Db	144173	ATCACCTTTGAGTGTGCTAATTTGTCGGTTGTTGTTTCCGTATCATAGAATAAAG	144114







QY	792	TGGGACTGGCTTACAGTTTTCGGACGTTTGTCCATGATATCATAGTGGGAAGCATGGCA	851
Db	78947	TGGGACTGGCTTACAGTTTTCGGACGTTTGTCCATGATATCATAGTGGGAAGCATGGCA	79006
QY	852	GCATCTAAGCAGACATGATGTTTGGAGAGGAGCTCAGATTTCTGCATCTTCATCTGCAAG	911
Db	79007	GCATCTAAGCAGACATGATGTTTGGAGAGGAGCTCAGATTTCTGCATCTTCATCTGCAAG	79066
QY	912	CAATAAAGGAGACTGTGTGSCACACTATACACAGCTTTGAACATAGGAGACCTCAAAAGCC	971
Db	79067	CAATAAAGGAGACTGTGTGSCACACTATACACAGCTTTGAACATAGGAGACCTCAAAAGCC	79126
QY	972	TGTTCCCAACAGTGAACAACTTCTCCCAACAGGTCATACCTCTTAATAAATACCAATTTCTT	1031
Db	79127	TGTTCCCAACAGTGAACAACTTCTCCCAACAGGTCATACCTCTTAATAAATACCAATTTCTT	79186
QY	1032	ATGAGGCAAGCAATTCAAAACACATGAGTCTATCAGAGGCGCCAAACCAATTCAAACCAACACAG	1091
Db	79187	ATGAGGCAAGCAATTCAAAACACATGAGTCTATCAGAGGCGCCAAACCAATTCAAACCAACACAG	79246
QY	1092	GTTTAAACAATTTGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCTTGGAGAGTAAGTAACAATT	1151
Db	79247	GTTTAAACAATTTGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCTTGGAGAGTAAGTAACAATT	79306
QY	1152	TAGATGAAGCAAGTCTCGGTATCAGGTCCTCAAAAGAAACTCAGGATGAATGGTCCACTGT	1211
Db	79307	TAGATGAAGCAAGTCTCGGTATCAGGTCCTCAAAAGAAACTCAGGATGAATGGTCCACTGT	79366
QY	1212	GGTTCCTATTACATCTGAAGACATGACCTCAGCTTACACGCTCCACCTCACTGACT	1271
Db	79367	GGTTCCTATTACATCTGAAGACATGACCTCAGCTTACACGCTCCACCTCACTGACT	79426
QY	1272	TCCCTTTCCCTAGCTCTCATTTCCAGGTAAACCTCGCCATTTTGGTAATGTGCTTCT	1331
Db	79427	TCCCTTTCCCTAGCTCTCATTTCCAGGTAAACCTCGCCATTTTGGTAATGTGCTTCT	79486
QY	1332	TGTTTCTTCTCTCCCTTCCCTCTCTTCTGGTCTTATCTTCTCTTCTTCTTCTTCTTCTTCT	1391
Db	79487	TGTTTCTTCTCTCCCTTCCCTCTCTTCTGGTCTTATCTTCTTCTTCTTCTTCTTCTTCT	79546
QY	1392	CGACGAGCTCTCTTAAAGGCTGAATCAGTCTGTAGTTCATGTTTAACTTCTACTACTTTC	1451
Db	79547	CGACGAGCTCTCTTAAAGGCTGAATCAGTCTGTAGTTCATGTTTAACTTCTACTACTTTC	79606
QY	1452	TCTCTGCTCTGGAATCATCCAGATGTCCTCGGCTGAGTCTCCCTCTTATCTCAATAAA	1511
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QY	1512	ACCTTTCCCTTAAACAGAAATGCAAAA	1539
Db	79667	ACCTTTCCCTTAAACAGAAATGCAACA	79694
RESULT 7			
AY165627			
LOCUS			
DEFINITION	AY165627 691 bp mRNA linear ROD 19-FEB-2003		
ACCESSION	Mus musculus decoy TRAIL receptor 2 long form (Dctraillr2) mRNA,		
VERSION	complete cds; alternatively spliced.		
KEYWORDS	AY165627		
SOURCE	AY165627.1 GI:27986023		
ORGANISM	Mus musculus (house mouse)		
REFERENCE	Mus musculus		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 691)		
TITLE	Schneider, P., Olson, D., Tardivel, A., Browning, B., Lugovskoy, A., Gong, D., Dobles, M., Herzig, S., Hofmann, K., Van Vlijmen, H., Hau, Y.-M., Burkle, L., Teschopp, J. and Zheng, T. S.		
JOURNAL	Identification of a New Murine Tumor Necrosis Factor Receptor Locus That Contains Two Novel Murine Receptors for Tumor Necrosis Factor-related Apoptosis-inducing Ligand (TRAIL) (TRAIL) J. Biol. Chem. 278 (7), 5444-5454 (2003)		







**COMMENT**

Baylor Plaza, Houston, TX 77030, USA  
 On Nov 15, 2002 this sequence version replaced gi:23603435.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: GOHM

Center clone name: CH230-229H15

----- Summary Statistics

Assembly program: Phrap; version 0.990329

Consensus quality: 225626 bases at least Q40

Consensus quality: 228934 bases at least Q30

Consensus quality: 231248 bases at least Q20

Estimated insert size: 233648; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

-----

\* NOTE: Estimated insert size may differ from sequence length  
 (see http://www.hgsc.bcm.tmc.edu/docs/Genbank\_draft\_data.html).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 2 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

\* 1 238590: contig of 238590 bp in length

\* 238591 238690: gap of unknown length

\* 238691 240262: contig of 1572 bp in length.

# FEATURES

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## ORIGIN

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Qy	570	AATGTGTGCGTGTGTGTTCTTCGTTATCAAGAAGATAAAGGTCTTACAGATGTTTCT	629
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Qy	630	TAGCTTCTCTTTTATTCATGAAGTGATATATGAGGGAACCTCTTTTATTTATTATT	689
Db	112656	TGGCTATCGTTTATTGTCATGAAGAAACACCATGGAGGCAACTCTTTTTTTTTTTTT	112597
Qy	690	TTATTTTA-----TTTTTATATGTTCTGAAC	715
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Db	112359	GCATCTTGATCTAAGTAGTCAAAAGGAGACTGTGTGCCATACCGGCAAAACTTGAGCA	112300
Qy	955	TAGGAGACCTCAAAAGCCTGTCCCACTAGTGACAAACTTC-----C	994
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Qy	1055	GAGTCTATGAGGCGCAAAACCAATTCAAACCAACACAGAGTTTAACAATTCCTCTGCAGCT	1114
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Qy	1115	CTCTGTGAGGCGCTCTCTTTGAGAGTAAGTAACAATTTAGATGAAGGCAAGTCTCT-GETA	1173
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Qy	1362	TGGTCTTACTTCTTCT	1421
Db	111821	TGGTCTTACTTCT	111776
Qy	1422	TCTGTAGTCTATGTTTAAATCTACTACTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1481
Db	111775	TCCTCTGGCAATGTTTAAATTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	111716





Db	501		-----GCTAATTGTCTTCTGTATCTGAAGAAGATAAGTTCTACAG	542
Qy	621	ATGTTTTCT-TAGCTTCCTCTTTTATTGC	646	
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LOCUS		Mus musculus TNP receptor family member SOB mRNA, complete cds.		
DEFINITION				
ACCESSION		AY046550		
VERSION		AY046550.1	GI:18056433	
KEYWORDS				
SOURCE		Mus musculus (house mouse)		
ORGANISM		Mus musculus		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;				
Pan,G., Mao,W. and Risse,P.				
TITLE		Characterization of SOB, a member of the TNFR family		
JOURNAL		Unpublished		
REFERENCE		2 (bases 1 to 531)		
AUTHORS		Pan,G.		
TITLE		Direct Submission		
JOURNAL		Submitted (18-JUL-2001) Molecular Oncology, Genentech, Inc, 1 DNA		
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Best Local Similarity		90.9%;	Pred. No. le-87;	Length 531;
Matches		428;	Conservative	0;
Mismatches		0;	Indels	0;
Gaps		0;		
Qy	81	GCTGCTGCTGCTGCTGTAATCTGCCCTTGCAAGTAAAATTTGCTATGCTAGAATT	140	
Db	39	GTTCTCTTGCTGCTGCTGTAATCTGTTCTTGCGGGTAAATTTTGTCTATGCTGGAATC	98	
Qy	141	ACACTCCTTCAAATGTCGCGCTGGTAATCTGTTCTAAAGACGCTCTGTTGCAAGACTG	200	
Db	99	ATATCTCTTCAACTGTCGCGATGGTGAATACCAGTCTAATGATGCTGTGTCAGAACCTG	158	
Qy	201	TTCTGCAGGTACATTTGTCAAGCGCCCTTGCAGAAATCCCCCATCTATCAAGGACAATGCA	260	
Db	159	TCCCTCAGGTACATTTGTCAAGCGCCCTTGCAAAATCCCCCATCTATCAAGGACAATGCA	218	
Qy	261	GAAGTGTCACCCAGGAAATTCACAGAGAAAGATAATTAATCTGGATGCTGTGTAATCTTTG	320	
Db	219	GAAGTGTCACCCAGGAAATTCACAGGAAAGATAATTAATGCGCTGCATGTTGTGAATCTTTG	278	
Qy	321	CTCCACCTGTGATAAGATCAGGAATGGTGGCCGACTGCTCAGCCACAGTGACCGGAA	380	
Db	279	CTCCACCTGTGATAAAGACCAAGATATGGTGCTGACTGTCTTGCCACAGTGACCGGAA	338	
Qy	381	ATGCCAGTGCCGAAACAGAGCTTTTACTTACTATCACCCCAAATTTCCAGAATCTGTCGCCCC	440	
Db	339	ATGGAGTGCCAAATAGGTCTTTACTACTATGACCCCAAATTTCCGGAATCATGCGCCC	398	
Qy	441	ATGTACCAAGTGTCCTCCTCCAGGAATCCCTGTCTCTCCAGGAATCCAATCTCAGAGCTAACAC	500	

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Result No.	Score	Query Match	Length	DB	ID	Description	
1	1550	100.0	1550	4	US-09-612-033B-7	Sequence 7, Appli	
2	1182.4	76.3	1509	3	US-09-411-722-3	Sequence 3, Appli	
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4	602	38.8	702	4	US-09-612-033B-9	Sequence 9, Appli	
5	514.6	33.2	1200	4	US-09-612-033B-13	Sequence 13, Appli	
6	412	26.6	412	4	US-09-612-033B-5	Sequence 5, Appli	
C 7	96.6	6.2	3791	3	US-08-675-773B-3	Sequence 3, Appli	
8	88.4	5.7	51259	3	US-08-817-891-209	Sequence 209, Appli	
9	88.4	5.7	51259	4	US-09-618-166-209	Sequence 209, Appli	
10	85.2	5.5	7218	1	US-08-232-463-14	Sequence 14, Appli	
11	81.4	5.3	30310	4	US-09-657-346A-96	Sequence 96, Appli	
C 12	78.6	5.1	3872	5	PCT-US93-12169-1	Sequence 1, Appli	
13	74.2	4.8	4243	3	US-08-477-831C-7	Sequence 7, Appli	
C 14	74.2	4.8	5257	4	US-09-917-254-47	Sequence 47, Appli	
15	74	4.8	90050	3	US-09-245-041-5	Sequence 5, Appli	
16	74	4.8	90050	4	US-09-358-055B-5	Sequence 5, Appli	
17	74	4.8	90050	4	US-09-893-238-5	Sequence 5, Appli	
C 18	55.2	3.6	872	4	US-09-509-712B-48	Sequence 48, Appli	
19	54	3.5	1225	4	US-09-569-098A-99	Sequence 99, Appli	
C 20	52.4	3.4	3611	2	US-08-727-118-1	Sequence 1, Appli	
C 21	50.6	3.3	113042	4	US-09-949-016-12343	Sequence 12343, A	
C 22	50.6	3.3	113042	4	US-09-949-016-15246	Sequence 15246, A	
C 23	48.8	3.1	325	2	US-08-531-927B-3	Sequence 3, Appli	
C 24	47.6	3.1	1776	2	US-08-531-927B-1	Sequence 1, Appli	
C 25	47.6	3.1	1776	3	US-09-441-886-12	Sequence 12, Appli	
C 26	47.6	3.1	2224	4	US-09-922-364A-44	Sequence 44, Appli	
C 27	47.6	3.1	2224	4	US-09-254-590-44	Sequence 44, Appli	



QY	561	GAGTGTGCTAAATTGTGTGCGTGTCTGTCTCTCCGTATCATTAAGAAGATAAAGGTTCTACAG	620
Db	521	-----GCTAATTCGTCTCTGTATCTGAAGAAGATAAAGGTTCTACAG	562
QY	621	ATGTTTTTCT-TAGCTTCCCTTTAATTCCTATGAAGTACTATGAGGGAACACTCTTTTAT	679
Db	563	ATGGTGTGTGTAGCTTCCCTTTAATGCTGTGAAGAGAAACCATGGAGGCAACTCT-----	617
QY	680	TTTATTTATTTTATTTATTTTATTTTAAATGCTTGAACTTTGATTTTGAAGACACAGGCTGGCCT	739
Db	618	-----TTCAATTTTATTTTATTTTATTTGATCTTGAACTTTGAGCACTGGAGCTGGACT	673
QY	740	CAAAATCACAGAGATCCAGACTAAGACAACTCTAAATAAGGGAACAATTTAATTTGGGACTG	799
Db	674	CAAACTCACAGAGATCCGGACTAGGCACCTCTAATATAGGAAACAATGGAATTTGGGACTG	733
QY	800	GCTTACAGTTTCGACGTTTTGTTCATGATATCATAGTGGGAGCATGCGACGACTTAA	859
Db	734	GCTTACAGTTTTCAGAGTTCTGTGCCATGATATCATAGTGGGAGCATGAGGCGACGGAG	793
QY	860	GCAGACATGATGTTGGAGAAGGAGCTGAGATTTCTGCATCTTGATCTGCAAGCAATAAAA	919
Db	794	GCACACATGTTGCTGGAGAAGAGCTGAGAGTTCTGCATCTTGATCTGCAAGCAATAAAA	853
QY	920	GGAGACTGTGTGCCACACTATACACAGCTTTGAACATAGGAGACCTCAAGGCTGTGCCCA	979
Db	854	GGAGACTGTGTGCCACACTACATAGCTTTGAACATAGGAGACCTCAAGGCTGTGCCCA	913
QY	980	CAGTGACAAACTTCTCTCAACAAGGTCATACCTCTTAATAATACCATTTCCTATGAGGCA	1039
Db	914	CAGTGACAAACTTCTCTCAACAAGGTCATACCTCTTAATAATACCATTTCCTATGAGGCA	973
QY	1040	AGCATTCAAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCAACACAGGTTAACAA	1099
Db	974	AGCATTCAAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCAACACAGGTTAACAA	1033
QY	1100	TTGCGCTCTGCAGCTCTCTGGTGAGGCGCCCTCCTTGAGAGTAAGTAAACAATTTAGATGAA	1159
Db	1034	TTGCGCTCTGCAGCTCTCTGGTGAGGCGCCCTCCTTGAGAGTAAGTAAACAATTTAGATGAA	1093
QY	1160	GGCAAGTCTGGTATCAGGTCCTCAAGAAAGAACTCAGGATGAATGGTCCACCTGTGGTTCCTA	1219
Db	1094	GGCAAGTCTGGTATCAGGTCCTCAAGAAAGAACTCAGGATGAATGGTCCACCTGTGGTTCCTA	1153
QY	1220	TTAACTACTGAGAAACATGACCTTCACCTTACAGCTCTCCACCTCCTCAGCTTCCCTTC	1279
Db	1154	TTAACTACTGAGAAACATGACCTTCACCTTACAGCTTCTCCACCTCCTCAGCTTCCCTTC	1213
QY	1280	CCTAGCTTCTCATTTCCAGGTAACCCCTGCCATTTTTTTGGTAATGTGCTTCTTTGGTTCTT	1339
Db	1214	CCTAGCTTCTCATTTCCAGGTAACCCCTGCCATTTTTTTGGTAATGTGCTTCTTTGGTTCTT	1273
QY	1340	CCTCTCTTTCCCTCTCTTCTGGTCCCTTACTTCTCTTCTCTCCACCTCTCCACAGC	1399
Db	1274	CCTCTCTTTCCCTCTCTTCTGGTCCCTTACTTCTCTCTCTCTCCACCTCTCCACAGC	1333
QY	1400	CTCCTCTTAAGGCGCTGAATCAGTCTGTAGGTCATGTTTTAATCTACTACTTTCTCTCTGCT	1459
Db	1334	CGCCTCTTAAGGCGCTGAATCAGTCTGTAGGTCATGTTTTAATCTACTACTTTCTCTCTGCT	1393
QY	1460	CTGGACTCATCCAGATGTCTCTGGCTGAGTCTCCCTCTATCTACAAATAAACCCCTTCC	1519
Db	1394	CTGGACTCATCCAGATGTCTCTGGCTGAGTCTCCCTCTATCTACAAATAAACCCCTTCC	1452
QY	1520	CCCTAACACAGAAATGCAAAA	1539
Db	1453	CCCTAACACAGAAATGGAACA	1472

### RESULT 3

RESUL 3  
US-09-855-266A-3

US-09-833-266A-3  
; Sequence 3, Application US/09855266A

```

; Patent No. 6784284
;
; GENERAL INFORMATION:
;
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
;
; FILE REFERENCE: 06501-040002
;
; CURRENT APPLICATION NUMBER: US/09/855,266A
;
; CURRENT FILING DATE: 2001-05-14
;
; PRIOR APPLICATION NUMBER: US 09/411,722
;
; PRIOR FILING DATE: 1999-10-01
;
; PRIOR APPLICATION NUMBER: PCT/JF98/01511
;
; PRIOR FILING DATE: 1998-04-01
;
; PRIOR APPLICATION NUMBER: JP 0/099653
;
; PRIOR FILING DATE: 1997-04-01
;
; NUMBER OF SEQ ID NOS: 13
;
; SOFTWARE: FastSeq for Windows Version 4.0
;
; SEQ ID NO 3
;
; LENGTH: 1509
;
; TYPE: DNA
;
; ORGANISM: Mus musculus
;
; FEATURE:
;
; NAME/KEY: CDS
;
; LOCATION: (12) ... (539)
;
; US-09-855-266A-3

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[illegible]





; CURRENT APPLICATION NUMBER: US/09/612,033B  
 ; CURRENT FILING DATE: 2000-07-07  
 ; PRIOR APPLICATION NUMBER: US 60/143,063  
 ; PRIOR FILING DATE: 1999-07-09  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 13  
 ; LENGTH: 1200  
 ; TYPE: DNA  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein  
 ; OTHER INFORMATION: consisting of Mus musculus sequences and  
 ; OTHER INFORMATION: Immunoglobulin sequences  
 ; NAME/KEY: CDS  
 ; LOCATION: (1)..(1194)  
 ; US-09-612-033B-13

	Query Match	33.2%	Score 514.6;	DB 4;	Length 1200;
	Best Local Similarity	96.5%;	Pred. No. 3.3e-138;		
	Matches 526;	Conservative 0;	Mismatches 19;	Indels 0;	Gaps 0;
QY	13	ATGTTTCGGCTTCTTCAGCGCTTGCTGCAGTCTGAGTGGCTGTGTTCCCTTTGGCGCGG	72		
Db	1	ATGTTTCGGCTTCTTCAGCGCTTGCTGCAGTCTGAGTGGCTGTGTTCCCTTTGGCGCGG	60		
QY	73	CTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGCTATG	132		
Db	61	CTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGCTATG	120		
QY	133	CTAGAATTACACTCCTTCAAATGTCCTGGCTGGTGAATACTGGTCTAAAGACGCTCTGTTGC	192		
Db	121	CTAGAATTACACTCCTTCAAATGTCCTGGCTGGTGAATACTGGTCTAAAGACGCTCTGTTGC	180		
QY	193	AAGAACTGTTCTGCAGGTACATTTGTCAAGCGCCCTGCGAATCCCCCATCTCAAGGA	252		
Db	181	AAGAACTGTTCTGCAGGTACATTTGTCAAGCGCCCTGCGAATCCCCCATCTCAAGGA	240		
QY	253	CAATGTGAGAAGTGTCAACCAGGAACAATTACAGAGAAAGATAATTACCTGGATGCTTGT	312		
Db	241	CAATGTGAGAAGTGTCAACCAGGAACAATTACAGAGAAAGATAATTACCTGGATGCTTGT	300		
QY	313	ATACTTTGCTCCACTGTGTATAAGATCAGAAATGTGGCGCATGTCTCAGCCACAGT	372		
Db	301	ATACTTTGCTCCACTGTGTATAAGATCAGAAATGTGGCGCATGTCTCAGCCACAGT	360		
QY	373	GACCGGAATGCCAGTCCGACAGAGTCTTTACTACTATGACCCCAAAATTTCCAGAACG	432		
Db	361	GACCGGAATGCCAGTCCGACAGAGTCTTTACTACTATGACCCCAAAATTTCCAGAACG	420		
QY	433	TGCCGCCCATGTACCAAGTGTCCCAGGAATCCCTGCTCTCAGGAATGCAACTCCACA	492		
Db	421	TGCCGCCCATGTACCAAGTGTCCCAGGAATCCCTGCTCTCAGGAATGCAACTCCACA	480		
QY	493	GCTAACACTGTGTGAGTTCATCTGTTTTCAAATCCCAAGAACCGCGTGTTCCTACTGTTA	552		
Db	481	GCTAACACTGTGTGAGTTCATCTGTTTTCAAATGTCGACACTCACACATGCCCAACCGTGC	540		
QY	553	TCACC 557			
Db	541	CCAGC 545			

RESULT 6  
 US-09-612-033B-5  
 ; Sequence 5, Application US/09612033B  
 ; Patent No. 6627199  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Saris, Chris  
 ; TITLE OF INVENTION: Isolation, Identification, and Characterization of  
 ; TITLE OF INVENTION: tmsc2, a No. 6627199 Member of the TNF-Receptor Superfamily  
 ; TITLE OF INVENTION: of Genes  
 ; FILE REFERENCE: 01017/35434A

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; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 412
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(411)
; OTHER INFORMATION: tmst2 00004-dl
US -09-612-033B-5

Query Match          26.6%; Score 412; DB 4; Length 412;
Best Local Similarity 100.0%; Pred.No.8e-109;
Matches 412; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy   1 TTGCACTCGGCCCATGTTTGGCTTCTTCTGCAGCTTGCGTGTCCAGTCTCGAGTCTGCGTTC 60
Db   1 TTGCACTCGGCCCATGTTTGGCTTCTTCTGCAGCTTGCGTGTCCAGTCTCGAGTCTGCGTTC 60

Qy   61 CTTTGGCGGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120
Db   61 CTTTGGCGGGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

Qy   121 AATTTTGCTATGCTAGAAATTACACTCCTCTCAAATGTCCCCCTGGTGAATACTGGTCTAAA 180
Db   121 AATTTTGCTATGCTAGAAATTACACTCCTCTCAAATGTCCCCCTGGTGAATACTGGTCTAAA 180

Qy   181 GAGCTCTGTTTGCAGAACAATGTTCTGCAGGTACATTTTGTCAAGCGGCCCTCGGAAATCCCC 240
Db   181 GAGCTCTGTTTGCAGAACAATGTTCTGCAGGTACATTTTGTCAAGCGGCCCTCGGAAATCCCC 240

Qy   241 CATACTCAAGCAACAATGTGAGAAGTGTCAACCAGGAACATTTCAAGAGAAGATAATTAC 300
Db   241 CATACTCAAGCAACAATGTGAGAAGTGTCAACCAGGAACATTTCAAGAGAAGATAATTAC 300

Qy   301 CTGATGCTTTGTATACTTTTCTGCTCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 360
Db   301 CTGATGCTTTGTATACTTTTCTGCTCACCTGTGATAAAGATCAGGAAATGGTGGCCGACTGC 360

Qy   361 TCAGCCACCAAGTGACCGGAAATGCCAGTCCGAAACAGGTCTTTTACTACTATG 412
Db   361 TCAGCCACCAAGTGACCGGAAATGCCAGTCCGAAACAGGTCTTTTACTACTATG 412


RESULT 7
US-08-675-773B-3/c
; Sequence 3, Application US/08675773B
; Patent No. 6166288
; GENERAL INFORMATION:
; APPLICANT: DIAMOND, LISA E
; APPLICANT: LOGAN, JOHN S
; APPLICANT: BYRNE, GUERARD W
; APPLICANT: SHARMA, AJAY
; TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC ANIMALS
; NUMBER OF INVENTION: FOR XENOTRANSPLANTATION...
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 419 SEVENTH STREET, N.W., SUITE 300
; CITY: WASHINGTON
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
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; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 1200
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
; NAME/KEY: CDS
; LOCATION: (1)..(1194)
US-09-612-033B-13

Query Match      33.2%; Score 514.6; DB 4; Length 1200;
Best Local Similarity 96.5%; Pred. No. 3.3e-138;
Matches 526; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

QY   13 ATGTTTCGGCTTCTTCAGCGTTGGTGTCAGACTGTGAGTCGCCTGTGGTCCCTTTGCGCGCGG 72
Db   1 ATGTTTCGGCTTCTTCAGCGTTGGTGTCAGACTGTGAGTCGCCTGTGGTCCCTTTGCGCGCGG 60

QY   73 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAAATCTGCCCTTGCAGGTAAAAATTGCTATG 132
Db   61 CTGCTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAAAATTGCTATG 120

QY   133 CTAGAATTACACCTCCTTTCAAATGTCCCCTGGTGGTAATACTGGTCTAAAGACGTCCTGTTGC 192
Db   121 CTAGAATTACACCTCCTTTCAAATGTCCCCTGGTGGTAATACTGGTCTAAAGACGTCCTGTTGC 180

QY   193 AAGAACTGTTCTGCAAGTACATTTGTCAAGCGCCCTGCGAATCCCCCATCTCAAGGA 252
Db   181 AAGAACTGTTCTGCAAGTACATTTGTCAAGCGCCCTGCGAATCCCCCATCTCAAGGA 240

QY   253 CAATGTGAGAAGTGTCAACCAGGAACAATTACAGAGAAAGATAATTACCTGGATGCTTGT 312
Db   241 CAATGTGAGAAGTGTCAACCAGGAACAATTACAGAGAAAGATAATTACCTGGATGCTTGT 300

QY   313 ATACTTTGCTCCACTGTGTATAAGATCAGAAAATGTGGCGCACTGTCTCAGCCACAGT 372
Db   301 ATACTTTGCTCCACTGTGTATAAGATCAGAAAATGTGGCGCACTGTCTCAGCCACAGT 360

QY   373 GACCGGAATGCCAGTCCGACGAGTCTTTACTACTATGACCCCAAAATTTCCAGAAATCG 432
Db   361 GACCGGAATGCCAGTCCGACGAGTCTTTACTACTATGACCCCAAAATTTCCAGAAATCG 420

QY   433 TGCCGCCCATGTACCAAGTGTCCTCAAGGAATCCCTGCTCTCACAGGAATGCAACTCCACA 492
Db   421 TGCCGCCCATGTACCAAGTGTCCTCAAGGAATCCCTGCTCTCACAGGAATGCAACTCCACA 480

QY   493 GCTAACACTGTGTGAGTTCACTGTTTTCAAATCCCAAGAACCGGCTGTTCTCTACTGTTA 552
Db   481 GCTAACACTGTGTGAGTTCACTGTTTTCAAATGTCGACACTCACACATGCCCAACCGTGC 540

QY   553 TCACC 557
Db   541 CCAGC 545

RESULT 6
US-09-612-033B-5
; Sequence 5, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Saria, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmsc2, a No. 6627199 Member of the TNF-Receptor Superfamily
; TITLE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
```



REFERENCE/DOCKET NUMBER: 240052.419C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 209:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 51259 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 209:  
US-09-618-166-209

Query Match 5.7%; Score 88.4; DB 4; Length 51259;  
Best Local Similarity 68.9%; Pred. No. 6.5e-14;  
Matches 182; Conservative 0; Mismatches 71; Indels 11; Gaps 4;

QY 750 GAGATCCAGACTAGACAACCTTAAT--AAGGGAACATTAAATGGGACCTGGCTTACAGT 808  
DB 3592 GACACCATGACTAGACAACCTCGATAGAAAGAAACATTTGATCAGGGCTGGCTTACAG 3651  
QY 809 TTGGAGCTTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTAAGCAGACATG 868  
DB 3652 TTGAGAGTTTGTGCTTATCA-----TGGAGGATGCGAGTGTACAGGCGAGCATG 3705  
QY 869 ATGTTGAGAGGAGCTGAGATTCTGCATCTTGTATCTGCAAGCAATAAAGGAGACTGT 928  
DB 3706 GTGCTGAGAGGAGCTGAGAGTTCTACATCCCAATTGGGGGCGAGGAGGAGAGA--GA 3763  
QY 929 GTGCCACACTATACAGCTTGAACATAGAGACCTCAGAGCTGTGCTCCACAGTGCACAA 988  
DB 3764 GTGAGACACTGTTGTGGCTGTAGCTTTGACACCTCAAGC--TCATCTGGTGACAT 3821  
QY 989 ACTTCTCCCAACAGGTCAACCT 1012  
DB 3822 ACTTCTCCCAACAGGCCACACT 3845

RESULT 10  
US-08-232-463-14  
Sequence 14, Application US/08232463  
Patent No. 5670367  
GENERAL INFORMATION:  
APPLICANT: DORNER, F.  
APPLICANT: SCHEIFLINGER, F.  
APPLICANT: FALKNER, F. G.  
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 1800 Diagonal Road, Suite 500  
CITY: Alexandria  
STATE: VA  
COUNTRY: USA  
ZIP: 22313-0299  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/232.463  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/935.313  
FILING DATE:  
APPLICATION NUMBER: EP 91 114 300.6  
FILING DATE: 26-AUG-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: BENT, Stephen A.  
REGISTRATION NUMBER: 29, 768  
REFERENCE/DOCKET NUMBER: 30472/114 IMM

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-9300  
TELEFAX: (703) 683-4109  
TELEX: 899149  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7218 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
CLONE: pTZgpt-Fls  
US-08-232-463-14

Query Match 5.5%; Score 85.2; DB 1; Length 7218;  
Best Local Similarity 3.7%; Pred. No. 1.6e-13;  
Matches 12; Conservative 216; Mismatches 94; Indels 0; Gaps 0;

QY 1202 GTTCCACTGGTTCCTATTAACTACTGAAGAATGACCTCACCTTACACGCTCTCCAC 1261  
DB 1048 GGTGAGGAGCTTGGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 1107  
QY 1262 CTCACTGACTTCCTTCCCTAGCTTCTCATTCAGGTAACCTGCAATTTTGTGTA 1321  
DB 1108 YY 1167  
QY 1322 TGTGCTTCTTGGTCTTCTCTCTCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1381  
DB 1168 YY 1227  
QY 1382 CTCCACTCTCCAGACCTCTCTTAAGGCTGAATCAGTCTGAGTCACTGTTAATC 1441  
DB 1228 YY 1287  
QY 1442 TACTACTTCTCTGCTCTGAGTCACTCAGATGCTCTGGCTGAGCTCTCCCTCTCTAT 1501  
DB 1288 YY 1347  
QY 1502 CTACAATAAACCTTCCCT 1523  
DB 1348 YYYYYYYYYYYYYYYYYYYY 1369

RESULT 11  
US-09-657-346A-96  
Sequence 96, Application US/09657346A  
Patent No. 6503754  
GENERAL INFORMATION:  
APPLICANT: Hong Zhang  
APPLICANT: Jacqueline Wyatt  
TITLE OF INVENTION: ANTISENSE MODULATION OF BH3 INTERACTING DOMAIN DEATH AGONIST  
TITLE OF INVENTION: EXPRESSION  
FILE REFERENCE: RTS-0135  
CURRENT APPLICATION NUMBER: US/09/657,346A  
CURRENT FILING DATE: 2000-09-07  
NUMBER OF SEQ ID NOS: 174  
SEQ ID NO 96  
LENGTH: 30310  
TYPE: DNA  
ORGANISM: Mus musculus  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (19791)...(19802)  
NAME/KEY: CDS  
LOCATION: (21160)...(21370)  
NAME/KEY: CDS  
LOCATION: (24168)...(24307)  
NAME/KEY: CDS  
LOCATION: (25696)...(25908)  
NAME/KEY: CDS  
LOCATION: (27235)...(27246)  
US-09-657-346A-96



Db 147 ATGCACTCCCTGGGCCAAGTA-TCAAACACACAAGTCTCTGAGGCGCCATTACTATCA 205  
Qy 1080 AAACACACACAGGTTTACAAT 1100  
Db 206 AACCTCCACCGTATCAAACT 226

RESULT 14  
US-09-917-254-47/c  
; Sequence 47, Application US/09917254  
; Patent No. 6703204  
; GENERAL INFORMATION:  
; APPLICANT: Mutter, George  
; APPLICANT: Baak, Jan  
; TITLE OF INVENTION: Prognostic Classification of Breast Cancer  
; FILE REFERENCE: B0801/7224(JRV)  
; CURRENT APPLICATION NUMBER: US/09/917,254  
; CURRENT FILING DATE: 2001-07-27  
; PRIOR APPLICATION NUMBER: US 60/222,093  
; PRIOR FILING DATE: 2000-07-28  
; NUMBER OF SEQ ID NOS: 102  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 47  
; LENGTH: 5257  
; TYPE: DNA  
; ORGANISM: Homo Sapiens  
US-09-917-254-47

Query Match 4.8%; Score 74.2; DB 4; Length 5257;  
Best Local Similarity 71.6%; Pred. No. 2e-10;  
Matches 111; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

Qy 771 CTAATAAGGGAACATTTAATTTGGGACTGGCTTACAGTTTCGGACGTTTTGTCCATGATT 830  
Db 5256 CTATAAGGGAAGCAATTTAATTTGGGCTGCTTACAG-TTCAGAGCTTCAGTCAATTATT 5198

Qy 831 ATCATAGTGGGAAGCATGGCAGCATCTAAGCAGACATGATGTTGGAGAAGGAGCTGAGAT 890  
Db 5197 GTCATGTTGGGAGGCATGGCAGCATGCAGGTAGACATCATTCAGAGGAGAGCAGAGAG 5138

Qy 891 TTCTGCATCTTGATCTGCAAGCATATAAGGAGAC 925  
Db 5137 TTCTACATCAGATTGGCAGGCTATGATCAGGGAC 5103

RESULT 15  
US-09-245-041-5  
; Sequence 5, Application US/09245041  
; Patent No. 6274339  
; GENERAL INFORMATION:  
; APPLICANT: Moore, K.  
; APPLICANT: Nagle, D.  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE DIAGNOSIS AND TREATMENT  
; FILE REFERENCE: 7853-136  
; CURRENT APPLICATION NUMBER: US/09/245,041  
; CURRENT FILING DATE: 1999-02-05  
; EARLIER APPLICATION NUMBER: 60/093,630  
; EARLIER FILING DATE: 1998-07-21  
; EARLIER APPLICATION NUMBER: 60/104,978  
; EARLIER FILING DATE: 1998-10-20  
; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 5  
; LENGTH: 90050  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-09-245-041-5

Query Match 4.8%; Score 74; DB 3; Length 90050;  
Best Local Similarity 76.9%; Pred. No. 1.3e-09;  
Matches 103; Conservative 0; Mismatches 30; Indels 1; Gaps 1;

Qy 771 CTAATAAGGGAACATTTAATTTGGGACTGGCTTACAGTTTCGGACGTTTTGTCCATGATT 830  
Db 47238 CTCTTACGAAGGACATTTAATTTGGGCTGCTTACAGTTTCAGAGGTTTAAATCCATTATC 47297  
Qy 831 ATCATAGTGGGAAGCATGGCAGCATCTAAGCAGACATGATGTTGGAGAAGGAGCTGAGAT 890  
Db 47298 ATCATGGCAGGAAGCATGGCAGCATTCAGGAGCATCGGTGCTGGAGGAGCCG-AGAGAG 47356

Qy 891 TTCTGCATCTTGAT 904  
Db 47357 TTCTATATCTTGAT 47370

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Job time : 783.13 secs

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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 16:10:01 ; Search time 3520.54 Seconds  
(without alignments)  
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Title: US-10-622-407-7  
Perfect score: 1550  
Sequence: 1 ttgcactggccatgttgg.....aatgcacaaaaaaaaa 1550

Scoring table: IDENTITY NUC  
Gapop 10\_0 , Gapext 1.0

Searched: 7351250 seqs, 323620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_NA.\*  
1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq.\*  
2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*  
3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*  
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5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*  
6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq.\*  
7: /cgn2\_6/ptodata/1/pubpna/US08\_NEW\_PUB.seq.\*  
8: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq.\*  
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11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*  
12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*  
13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*  
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17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*  
18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*  
19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*  
20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*  
21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*  
22: /cgn2\_6/ptodata/1/pubpna/US10\_NEW\_PUB.seq.\*  
23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*  
24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*  
25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*  
26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1550	100.0	1550	17	US-10-622-407-7
2	1182.4	76.3	1509	9	Sequence 7, Appli
3	1182.4	76.3	1509	19	Sequence 3, Appli
4	709.4	45.8	967	14	Sequence 7, Appli
5	602	38.8	702	17	Sequence 9, Appli
6	514.6	33.2	1200	17	Sequence 13, Appli
7	412	26.6	412	17	Sequence 5, Appli

	8	392	25.3	415	9	US-09-728-445-737	Sequence 737, App
	9	392	25.3	415	22	US-10-964-549-737	Sequence 737, App
	10	253.2	16.3	357	14	US-10-193-616-5	Sequence 5, Appli
C	11	205.6	13.3	124289	13	US-10-087-192-817	Sequence 817, App
	12	191.6	12.4	203070	13	US-10-087-192-247	Sequence 247, App
	13	187.6	12.1	721377	21	US-10-461-862-163	Sequence 163, App
	14	187	12.1	111836	19	US-10-322-281-51	Sequence 51, Appl
	15	186	12.0	16940	22	US-10-942-954-2	Sequence 2, Appl1
	16	182.2	11.8	35425	19	US-10-322-696-91	Sequence 91, Appl
	17	178.2	11.5	71057	13	US-10-087-192-409	Sequence 409, App
	18	168.6	10.9	56587	13	US-10-087-192-1687	Sequence 1687, Ap
	19	167.4	10.8	27299	13	US-10-087-192-937	Sequence 937, App
	20	166.4	10.7	134442	21	US-10-461-862-23	Sequence 23, Appl
C	21	166.2	10.7	121429	13	US-10-322-281-587	Sequence 587, App
	22	164	10.6	203070	13	US-10-087-192-247	Sequence 247, App
	23	161.4	10.4	150351	19	US-10-322-281-453	Sequence 453, App
	24	160.8	10.4	151858	19	US-10-322-281-653	Sequence 653, App
	25	159.6	10.3	51281	11	US-09-997-722-139	Sequence 139, App
	26	158.6	10.2	29222	17	US-10-085-117-349	Sequence 349, App
C	27	154.8	10.0	117382	13	US-10-087-192-1435	Sequence 1435, Ap
C	28	154.8	10.0	659158	9	US-09-771-208-20	Sequence 20, Appl
	29	154	9.9	89756	21	US-10-461-862-133	Sequence 133, App
	30	153.6	9.9	122859	13	US-10-087-192-37	Sequence 37, Appl
	31	150.6	9.7	65253	17	US-10-085-117-331	Sequence 331, App
	32	150.6	9.7	185555	13	US-10-087-192-1999	Sequence 1999, Ap
C	33	150.4	9.7	37923	13	US-10-087-192-1891	Sequence 1891, Ap
	34	149	9.6	1900	21	US-10-764-420-905	Sequence 905, App
	35	146.6	9.5	219715	20	US-10-417-375-63	Sequence 63, Appl
	36	146.4	9.4	45736	19	US-10-322-281-767	Sequence 767, App
C	37	146	9.4	54669	11	US-10-322-281-347	Sequence 347, App
	38	145.6	9.4	41637	11	US-09-997-722-103	Sequence 103, App
C	39	144.4	9.3	66499	19	US-10-322-281-39	Sequence 39, Appl
	40	143.2	9.2	38142	20	US-10-417-375-55	Sequence 55, Appl
C	41	142.4	9.2	63502	13	US-10-087-192-271	Sequence 271, App
C	42	142.4	9.2	177249	17	US-10-085-117-223	Sequence 223, App
	43	142	9.2	57561	13	US-10-087-192-1129	Sequence 1129, Ap
	44	141.8	9.1	608916	21	US-10-461-862-1	Sequence 1, Appli
C	45	140	9.0	38977	13	US-10-087-192-1321	Sequence 1321, Ap

ALIGNMENTS

RESULT 1  
US-10-622-407-7  
; Sequence 7, Application US/10622407  
; Publication No. US20040018544A1  
; GENERAL INFORMATION:  
; APPLICANT: Saris, Chris  
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL  
; FILE REFERENCE: 01017/35434B  
; CURRENT APPLICATION NUMBER: US/10/622,407  
; CURRENT FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: US 09/612,033  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/143,063  
; PRIOR FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 1550  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (13)..(606)  
; FEATURE:  
; OTHER INFORMATION: mouse tmst2  
US-10-622-407-7

Query Match 100.0%; Score 1550; DB 17; Length 1550;  
Best Local Similarity 100.0%; Pred. No. 0;



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QY 201 TTCTGAGGTACATTTGTCAAGGGCCCTCGGAAATCCCCCATACTCAAGGACAATGTGA 260
DB 170 TCCCTCAGGTACATTTGTCAAGGGCCCTCGGAAATCCCCCATACTCAAGGACAATGTGA 229
QY 261 GAAGTGTCAACCCAGGAACATTTCACAGAGAAGATAATTAATCTGGATCTTGTATCTTTG 320
DB 230 GAAGTGTCAACCCAGGAACATTTCACAGGAAGAATATATGGCTGCTGATGATTTGTGACTTTG 289
QY 321 CTCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGTCTAGCCACCAAGTGAACCGGAA 380
DB 290 CTCACCTGTGATAAAGACAGGAATATATGGTGGCTGACTGTCTGCCACCAAGTGAACCGGAA 349
QY 381 ATGCCAGTGGCAACAGCTCTTACTACTATGATGCCCAAAATTTCCAGAAATCGTGGCGCCC 440
DB 350 ATGCCAGTGGCAAAATAGTCTTTACTACTATGATGCCCAAAATTTCCGGAATCATGGCGCCC 409
QY 441 ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATCAACTCCACAGCTAACAC 500
DB 410 ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACAGCTAACAC 469
QY 501 TGTGTGAGTTCATCTCTTTCAATCCAGAAACCGGCTGTCTCTACTGTTATCACCTTT 560
DB 470 TGTGTGAGTTCATCTCTTTCAATCCAGAACTGGCTGTCTCTACTGAT----- 520
QY 561 GAGTGTGCTAAATTGTGTCTGTTGTCTTCCTCGTATCATTAAGAAGATAAAAGGTTCTACAG 620
DB 521 -----GCTAATTTGTCTTCTGTATCTGAAGAAGATAAAAGGTTCTACAG 562
QY 621 ATGTTTCT--TAGCTTCCTTTTATGCTATGAAGTATCTATGGAGGCACTCTTTAT 679
DB 563 ATGTTGTCTAGTCTCTTTTATGCTGAAGAAACCATGGAGGCACTCT----- 617
QY 680 TTTATTTATTTATTTTATTTTAAATGTCTGAACCTTGATTTGAAGACCAAGGCTGGCCT 739
DB 618 ----TTCAATTTTATTTTAAATGTCTGAACCTTGATTTGAAGACCAAGGCTGGACT 673
QY 740 CAAATCACAGATCCAGACTAAGACAACCTTAATAAGGAAACATTAAATTTGGGACTG 799
DB 674 CAAACTCACAGATCCGACTAGGCACCTTAATAATAGGAAACATTGAATTTGGGACTG 733
QY 800 GCTTACAGTTTCGACGCTTTGTCATGATATCATAGTGGGAAGCATGCGACATCTAA 859
DB 734 GCTTACAGTTTCGACGCTTTGTCATGATATCATAGTGGGAAGCATGAGGACGAG 793
QY 860 GCAGACATGATTTGGAGAAGGAGCTGAGATTTCTGCATCTTGATCTGCAAGCAATAAAA 919
DB 794 GCACACATGCTGTGGAGAAGAGCTGAGATTTCTGCATCTTGATCTGCAAGCAATAAAA 853
QY 920 GGAGACTGTGTGCACACTATACACAGCTTGAAATAGGAGACTCAAGCCTGTCCCA 979
DB 854 GGAGACTGTGTGCACACTACACATAGCTTGAACATAGGAGACTCAAGCCTGTCCCA 913
QY 980 CAGTGACAAATCTCTCCACNAGGTATACCTCTTAATAATACCAATTTCTATGAGCA 1039
DB 914 CAGTGACAAATCTCTCTCCACNAGGTATACCTCTTAATAATACCAATTTCTATGAGCA 973
QY 1040 AGCAATCAAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCAACAGGTTAACAA 1099
DB 974 AGCAATCAAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACCAACAGGTTAACAA 1033
QY 1100 TTGCCCTCTCAGCTCTCTGTGTGAGGCCCCTCTCTTGAGAGTAAGTAAATAATTTAGATGAA 1159
DB 1034 TTGCCCTCTCAGCTCTCTGTGTGAGGCCCCTCTCTTGAGAGTAAGTAAATAATTTAGATGAA 1093
QY 1160 GGCNAGTCTCTGATCAGGTCCAAAGAACTCAGGATGAATGGTCACTGTGGTCTCTA 1219
DB 1094 GGCNAGTCTCTGATCAGGTCCAAAGAACTCAGGATGAATGGTCACTGTGGTCTCTA 1153
QY 1220 TTAACATCTGAAAGAACATGACCTCTACAGTCTCCACCTCTACGACTTCCCTTCC 1279
DB 1154 TTAACATCTGAAAGAACATGACCTCTACAGTCTCCACCTCTACGACTTCCCTTCC 1213
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QY 1280 CCTAGCTTCTCATTTCCAGGTAACCTTGCCATTTTGGTAATGTGTGCTTCTTGGTTCTT 1339
DB 1214 CCTAGCTTCTCATTTCCAGGTAACCTTGCCATTTTGGTAATGTGTGCTTCTTGGTTCTT 1273
QY 1340 CTTCTCTTTTCCCTCTCTCTTCTGGTCTTACTTCTTCTCTCTCCCTCCCACTCTCCACCAGC 1399
DB 1274 CTTCTCTTTTCCCTCTCTCTTCTGGTCTTACTTCTTCTCTCTCTCCCTCCCACTCTCCACCAGC 1333
QY 1400 CTCTCTTTAAGGCTGAATCAGTCTGTAGTGTATGTTTAAATCTACTTCTTCTCTCTGCT 1459
DB 1334 CGCTCTTTAAGGCTGAGTCTGTGAGGCTATGTCAGGCAATGTTTAACTACTTCTTCTCTGCT 1393
QY 1460 CTGCACTCATCCAGATGTCTCTGCTGAGCTCTCCCTCTCTATCTACAAATAAAACCTTCC 1519
DB 1394 CTGCACTCATCCAGATGTCTCTGCTGAGCTCTCCCTCTCTATCTACAAATAAA--CCTTCC 1452
QY 1520 CCCTAACCCAGAAATGCAAAA 1539
DB 1453 CCCTAACCCAGAAATGGAACA 1472

RESULT 3
US-10-802-332-3
; Sequence 3, Application US/10802332
; Publication No. US20040152879A1
; GENERAL INFORMATION:
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/10/802,332
; PRIOR FILING DATE: 2004-03-16
; PRIOR APPLICATION NUMBER: US/09/855,266
; PRIOR FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1509
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (12)...(539)
US-10-802-332-3

Query Match 76.3%; Score 1182.4; DB 19; Length 1509;
Best Local Similarity 90.5%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 101; Indels 38; Gaps 4;

QY 81 GCTGTGCTGCTGCTGCTGCTGAATCTGCCCTTGAGGTAAATTTGCTATGCTAGAAATT 140
DB 50 GTTCTCTTGTGCTGCTGCTGAATCTGTTCTTGGCGGTAAATATTGCTATGCTGAATC 109
QY 141 ACACCTCTTCAATGTCCCGCTGGTGAATCTGTTCTAAAGAGCTGTTTGCAGAACTG 200
DB 110 ATACTCTTCACTGTCCCGATGGTGAATACCAGTCTAATGATGTCTGTGTCGAAGACTG 169
QY 201 TTCTGCAAGGTACATTTTGTCAAGGCGCTCGGAAATCCCCCATACTCAAGGACAATGTGA 260
DB 170 TCCTCAGGTACATTTTGTCAAGGCGCTCGGAAATCCCCCATACTCAAGGACAATGTGA 229
QY 261 GAAGTGTCAACCCAGGAACATTTCACAGAGAAGATAATTAATCTGGAATGCTTGTATCTTTG 320
DB 230 GAAGTGTCAACCCAGGAACATTTCACAGGAAAGATAATGGCTGCTGATGATTTGAACTTTG 289
QY 321 CTCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGTCTAGCCACCAAGTGAACCGGAA 380
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561	Qy	GAGTGTCTAAATTGTGTCGGTTTGTGCTCCGTATCATATGAAGATATAAAGGTTCTTACAG	520
515	Db	-----TAAATTGTCTTCTGTATCTGAGAGAGATAAAGGTTCTTACAG	554
621	Qy	ATGCTTTTCT-TAGCTTCCCTTTTATTTGCTATCAAGTGTATCTATCTGAGGCGAACTCTTTTAT	679
555	Db		612
680	Qy	TTTATTATTTTATTATTTTATTTTAACTCTTTGAACCTTGAATTTGAAGACCAGGCTGGCCT	739
613	Db		665
740	Qy	CAAAATCAAGAGATCCGAGCTTAAGACAACTCTAATAAGGGAACATTTTAATTTGGGACTG	799
666	Db		725
800	Qy	GCTTACAGTTTCGGAGCTTTTGTCCATGATTTATCATAGTGGGAAGCATGCGACATCTTAA	859
726	Db		785
860	Qy	GCAGACATGATTTGTGGAGAGAGAGCTGAGATTTCTGCAATCTTGATCTCGAAGCAATAAAA	919
786	Db		845
920	Qy	GGAGACTGTGTGCCACACTATACACAGCTTGAACATAGGAGACCTCAAAGCCTGTCCCCA	979
846	Db		905
980	Qy	CAGTGAACAACTTCTCCCAACAGGTCATACCTCTCTAATAATACCATTTCTTATGAGGC	1038
906	Db		964

## RESIST 5

; Sequence 9, Application US/10622407  
 ; Publication No. US20040018544A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Saxis, Chris  
 ; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TNST2, A NOVEL  
 ; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

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1  TITLE OF INVENTION:  MEMBER OF THE INF-RECEPTOR SUPERFAMILY OF GENES
2
3  FILE REFERENCE:  01017/35434B
4
5  CURRENT APPLICATION NUMBER:  US/10/622,407
6
7  CURRENT FILING DATE:  2003-07-17
8
9  PRIOR APPLICATION NUMBER:  US 09/612,033
10
11 PRIOR FILING DATE:  2000-07-07
12
13 PRIOR APPLICATION NUMBER:  US 60/143,063
14
15 PRIOR FILING DATE:  1999-07-09
16
17 NUMBER OF SEQ ID NOS:  15
18
19 SOFTWARE:  PatentIn Ver. 2.0
20
21 SEQ ID NO 9
22
23 LENGTH:  702
24
25 TYPE:  DNA
26
27 ORGANISM:  Mus musculus
28
29 FEATURE:
30
31 NAME/KEY:  CDS
32
33 LOCATION:  (13)..(552)
34
35 FEATURE:
36
37 OTHER INFORMATION:  Primer 2086-39
38
39 US-10-622-407-9
40

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	Query Match	38.8%;	Score 602;	DB 17;	Length 702;	
	Best Local Similarity	93.6%;	Pred. No. 5.5e-15;			
	MATCHES 657;	Conservative	0;	Mismatches	0; Indels	45; Gaps
						1.
Qy	1	TTGCACTCGGCAGATTGGCTTCTTCGTGACAGCTTGTTGTCACAGTCTCAGTGCCTGGTTC	60			
Dd	1	TTGCACTCGGCACATTTTGGCTTCTTCGTGACAGTCTTGTTGTCACAGTCCAGTCCGCTGGTTC	60			
Qy	61	CTTTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTCGAGATA	120			
Dd	61	CTTTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCCTTCGAGATA	120			

Qy	121	AAATTTGCTATGCTAGAAATTACACTCTTTCAAAATGTCCTGGTGGTAATCTAGTCTCTAAA	181
Db	121	AAATTTGCTATGCTAGAAATTAACCTCTCTTCAAATGTCCCGTGGTGGAAATCTGGTCTAAA	180
Qy	181	GAGTCTGTTTGCAGAAACTGTTCTGTCAGGTACATTTGTCAAGCGCCCTTGCAGAAATCCCC	240
Db	181	GAGTCTGTTTGCAGAAACTGTTCTGTCAGGTACATTTGTCAAGCGCCCTTGCAGAAATCCCC	240
Qy	241	CATACCTCAAGSACAATGTGAAGAGTGTCACCCAGSACATTTCAACAGAGAAAGATAAATTAC	300
Db	241	CATACCTCAAGSACAATGTGAAGAGTGTCACCCAGSACATTTCAACAGAGAAAGATAAATTAC	300
Qy	301	CTGGAATGCTGTATACCTTTTGCTCCACTGTGATTAAGATCAGGAATGGTGCCTGCAGCTGC	360
Db	301	CTGGAATGCTGTATACCTTTTGCTCCACTGTGATTAAGATCAGGAATGGTGCCTGCAGCTGC	360
Qy	361	TCAGCCACCACTGACCCGNAATGCCAGTGCCGAAACAGGTCTTTTACTACTATGACCCAAAA	420
Db	361	TCAGCCACCACTGACCCGNAATGCCAGTGCCGAAACAGGTCTTTTACTACTATGACCCAAAA	420
Qy	421	TTTTCCAGAATCGTGCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCTCTCCAGGAA	480
Db	421	TTTTCCAGNAATCGTGCGCCCATGTACCAAGTGTCCCCAAGGAATCCCTGTCTCTCCAGGAA	480
Qy	481	TGCAACTCTCCACAGCTAACACATGTGTGTCAGTTTCATCTGTTTTCAGSAGATCTGCCTCAGTG	540
Db	481	TGCAACTCTCCACAGCTAACACATGTGTGTCAGTTTCATCTGTTTTCAGSAGATCTGCCTCAGTG	540
Qy	524	-----ATCCCGAAGAACCGCTGTCTCTACTGTTTATCA	555
Db	541	GCCTGGCCCTATCTGAAATGGTTTCAACAGATCCCGAAGAACCGCTGTCTCTACTGTTTATCA	600
Qy	556	CCTTTGAGTGTGCTAAATTTGTTGTCCTGTTGTTCTTCCGTATCATTAAGAGATAAAGGTTTC	615
Db	601	CCTTTGAGTGTGCTAAATTTGTTGTCCTGTTGTTCTTCCGTATCATTAAGAGATAAAGGTTTC	660
Qy	616	TACAGATGTTTTCTTAGCTTCCCTTTTATGTCTATGAAGTGAT	657
Db	661	TACAGATGTTTTCTTAGCTTCCCTTTTATGTCTATGAAGTGAT	702

## RESULT 6

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US-10-622-407-13
Sequence 13, Application US/10622407
Publication No. US20040018544A1
GENERAL INFORMATION:
APPLICANT: Saris, Chris
TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
TITLE OF INVENTION: MEMBER OF THE TNP-RECEPTOR SUPERFAMILY OF GENES
FILE REFERENCE: 01017/35434B
CURRENT APPLICATION NUMBER: US/10/622,407
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US 09/612,033
PRIOR FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: US 60/143,063
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO 13
LENGTH: 1200
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
OTHER INFORMATION: consisting of Mus musculus sequences and
OTHER INFORMATION: Immunoglobulin sequences
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1194)
US-10-622-407-13

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Query Match 33.2%; Score 514.6; DB 17; Length 1200;





Db 190 CTGGATGCTTGTATATCTTTGCTCACCCTGTGATTAAGATCAGGAATGGTGGCGACTGC 249  
Qy 361 TCAGCCACCAAGTACCGGAAATGCCAGTGGCGAACAGGTCTTTACTACTATGACCCAAAA 420  
Db 250 TCAGCCACCAAGTACCGGAAATGCCAGTGGCGAACAGGTCTTTACTACTATGACCCAAAA 309  
Qy 421 TTTCCAGAAATCGTGGCGCCCATGTATACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAA 480  
Db 310 TTTCCAGAAATCGTGGCGCCCATGTATACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAA 369  
Qy 481 TGCACCTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCAAA 524  
Db 370 TGCACCTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCAAA 413

RESULT 9  
US-10-964-549-737  
; Sequence 737, Application US/10964549  
; Publication No. US20050186677A1  
; GENERAL INFORMATION:  
; APPLICANT: Friederich, Glenn  
; APPLICANT: Zambrowicz, Brian  
; APPLICANT: Sands, Arthur T.  
; TITLE OF INVENTION: Novel Mutated Mammalian Cells and Animals  
; FILE REFERENCE: LEX-0286-USA  
; CURRENT APPLICATION NUMBER: US/10/964,549  
; PRIOR FILING DATE: 2004-10-13  
; PRIOR APPLICATION NUMBER: US/09/750,456  
; PRIOR FILING DATE: 2000-12-28  
; PRIOR APPLICATION NUMBER: US 09/728,445  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/169,358  
; PRIOR FILING DATE: 1999-12-01  
; NUMBER OF SEQ ID NOS: 891  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 737  
; LENGTH: 415  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-10-964-549-737

Query Match 25.3%; Score 392; DB 22; Length 415;  
Best Local Similarity 99.8%; Pred. No. 7.3e-98;  
Matches 403; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 121 AAATTTGCTATGCTAGAAATACACTCTTCAAATGTCCTGGTGAATACTGTCTTAAA 180  
Db 11 AAATTTGCTATGCTAG-ATTACACTCTTCAAATGTCCTGGTGAATACTGTCTTAAA 69  
Qy 181 GACGTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTCGAAATCCCC 240  
Db 70 GACGTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCAAGGCGCCCTCGAAATCCCC 129  
Qy 241 CATACTCAAGACAATGTGAGAAGTGTACCCAGGAACATTCACAGAGAAAGATAATTAC 300  
Db 130 CATACTCAAGACAATGTGAGAAGTGTACCCAGGAACATTCACAGAGAAAGATAATTAC 189  
Qy 301 CTGGATGCTGTATATCTTTGCTCCACCTGTGATTAAGATCAGGAATGGTGGCGACTGC 360  
Db 190 CTGGATGCTGTATATCTTTGCTCCACCTGTGATTAAGATCAGGAATGGTGGCGACTGC 249  
Qy 361 TCAGCCACCAAGTACCGGAAATGCCAGTGGCGAACAGGTCTTTACTACTATGACCCAAAA 420  
Db 250 TCAGCCACCAAGTACCGGAAATGCCAGTGGCGAACAGGTCTTTACTACTATGACCCAAAA 309  
Qy 421 TTTCCAGAAATCGTGGCGCCCATGTATACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAA 480  
Db 310 TTTCCAGAAATCGTGGCGCCCATGTATACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAA 369  
Qy 481 TGCACCTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCAAA 524  
Db 370 TGCACCTCCACAGCTAACACTGTGTGCAGTTCATCTGTTTCAAA 413

RESULT 10  
US-10-193-616-5  
; Sequence 5, Application US/10193616  
; Publication No. US20030096355A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Ke  
; TITLE OF INVENTION: Isolation, Identification, and Characterization of  
; TITLE OF INVENTION: ymz5, a novel  
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family  
; FILE REFERENCE: 01017/35551A  
; CURRENT APPLICATION NUMBER: US/10/193,616  
; CURRENT FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: US/09/611,989  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/143,137  
; PRIOR FILING DATE: 1999-07-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 357  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (6)..(356)  
US-10-193-616-5

Query Match 16.3%; Score 253.2; DB 14; Length 357;  
Best Local Similarity 87.9%; Pred. No. 2.1e-59;  
Matches 276; Conservative 0; Mismatches 38; Indels 0; Gaps 0;

Qy 81 GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGCTATGCTAGAAATT 140  
Db 44 GTTCTCTTGTGCTGCTGCTGAATCTGTTCTTGGCGGTAATATTTGCTATGCTGAATC 103  
Qy 141 ACACCTCTTCAAATGTCCCGTGGTGAATCTGTTTAAAGAGCTGTTTGCAGAACTG 200  
Db 104 ATACTCTTCAACTGTCCCGATGGTGAATACCACTCTTAATGATGTCTGTTGCAAGACTG 163  
Qy 201 TTCTGCAGGTACATTTGTCAAGCGCCCTCGGAAATCCCCCATACTCAAGACAATGTGA 260  
Db 164 TCCTCAGGTACATTTGTCAAGCGCCCTCGCAAAATCCCCCATACTCAAGACAATGTGA 223  
Qy 261 GAAGTGTACCCAGGAACATTCACAGAGAAAGATAATTAATCTGGATGCTTGTATCTTTG 320  
Db 224 GAAGTGTACCCAGGAACATTCACAGAGAAAGATAATTAATGCGCTGCTGATGATTGTGA 283  
Qy 321 CTCACCTGTGATAAAGATCAGGAATGGTGGCGACTGCTCAGCCACGATGACCGGAA 380  
Db 284 CTCACCTGTGATAAAGACCAAGATATGGTGGCTGACTGTTCTGCCACCAGTGACCGGAA 343  
Qy 381 ATGCCAGTGGCGAA 394  
Db 344 ATGCCAGTGGCGAA 357

RESULT 11  
US-10-087-192-817/c  
; Sequence 817, Application US/10087192  
; Publication No. US20020182586A1  
; GENERAL INFORMATION:  
; APPLICANT: Morris, David W.  
; APPLICANT: Engelhard, Eric K.  
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR  
; TITLE OF INVENTION: CANCER  
; FILE REFERENCE: 529452000122  
; CURRENT APPLICATION NUMBER: US/10/087,192  
; CURRENT FILING DATE: 2002-03-01  
; PRIOR APPLICATION NUMBER: US 09/747,377  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: US 09/798,586  
; PRIOR FILING DATE: 2001-03-02

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; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 817
; LENGTH: 124289
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(124289)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-817

Query Match      13.3%; Score 205.6; DB 13; Length 124289;
Best Local Similarity 75.3%; Pred. No. 8.9e-45;
Matches 256; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 755 CCAGCTAAGACAACTCTAATAAGGGAACATTTAATTGGGACTTGGCTTACAGTTTCGGA 814
Db 32622 CCAGCTAAGACAACTTTTATAAAGAAACATTTAATCTGGGAATGGCTTACAGTTTCGA 32563

Qy 815 CGTTTGTCCATGATTATCATATAGTGGGAAGCATGGCAGCATCTTAAGCAGACATGATGTTG 874
Db 32562 AGTTTAGTCCATTATCATATGGCAGGAAGCATGGCAGTATCCAGGCAGAAATGGTGTG 32503

Qy 875 GAGAGGAGCTGAGATTTCGATCTTGATCTGCAAGCAATAAAGGAGAGCTGTGTGCA 934
Db 32502 GAGAAAGGTTTGACAGATTCTACATATTGATCTGAAGGCAGCAGAAAGGGGATTTGTTCCA 32443

Qy 935 CACTATACACAGCTTGAACATAGAGACCTCAAAGCCCTGCCCCACAGTGCACAACTTCC 994
Db 32442 CACTGGTGGAGCTTGACATAGAGGCTTAAAGCTTGTCTTCAATGATACATTTCT 32383

Qy 995 TCCAAACAGGTATACCTCTTAATAATACCAATTTCTTATGAGGCAAGCATTTCAACACAT 1054
Db 32382 TCCAAATATGTTCTCACCTCTTAATAATGCTACTCCCTATGSGCCAAACATTTCAAAGCAT 32323

Qy 1055 GAGTCTATGAGGCGCAACCAATTCACACACACAGGTT 1094
Db 32322 GATTCTATAGGGGTACATACCTATTTCAGAGCACCACAGATT 32283

RESULT 12
US-10-087-192-247
; Sequence 247, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; PRIOR FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 247
; LENGTH: 203070
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(203070)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-247

Query Match      12.4%; Score 191.6; DB 13; Length 203070;
Best Local Similarity 75.4%; Pred. No. 8.9e-41;
Matches 264; Conservative 0; Mismatches 84; Indels 2; Gaps 2;

; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 817
; LENGTH: 124289
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(124289)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-817

Query Match      12.1%; Score 187.6; DB 21; Length 721377;
Best Local Similarity 77.8%; Pred. No. 2.3e-39;
Matches 252; Conservative 0; Mismatches 69; Indels 3; Gaps 2;

Qy 747 ACAGAGATCCAGACTAAGACAACTCTAAT-AAGGGAACATTTAATTGGGACTGGCTTAC 805
Db 193445 AGAGACACCATGACCATGGCACTCTTAAAGGGAACATTTAATTGGGACTGGCTTAC 193504

Qy 806 AGTTTCGAGCGTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTTAAGCAGAC 865
Db 193505 AGTTTCGAGCGTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTTAAGCAGAC 193564

Qy 866 ATGATGT--TGGAGAGGAGCTGAGATTCTTGGATCTTGTATCTGCAAGCAATAAAGGAG 923
Db 193565 ATGATGT--TGGAGAGGAGCTGAGATTCTTGGATCTTGTATCTTATCCACAGGCAACAGAGAG 193624

Qy 924 ACTGTGTGCCACACTATACACAGCTTGAACATAGGAGACCTCAAAGGCTGTGCCACAGT 983
Db 193625 ACTATAAGCCACACTGGGCATTAAGTGGACATGACATTAAGGCTGTGCCACAGT 193684

Qy 984 GACAACTTCTCTCAACAAGGTGATACCTCTCTTAATAATACATTTCTTATGAGGCAAGCA 1043
Db 193685 GACAACTTCTCTCAACAAGGTCACCTCTCTTAATAGTGCCTCTCTATGAGGCAAGCA 193744

Qy 1044 TTCAACACATGATGCTTATGAGG 1067
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Db 193745 TTCAACATATGAGTCTAAGGGGG 193768
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RESULT 14
US-10-322-281-51
; Sequence 51, Application US/10322281
; Publication No. US20040126762A1
; GENERAL INFORMATION:
; APPLICANT: David W. Morris
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer
; FILE REFERENCE: 529452001000
; CURRENT APPLICATION NUMBER: US/10/322,281
; CURRENT FILING DATE: 2002-12-17
; NUMBER OF SEQ ID NOS: 866
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 111836
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(111836)
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-51

Query Match 12.1%; Score 187; DB 19; Length 111836;
Best Local Similarity 78.8%; Pred. No. 1.2e-39;
Matches 223; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

Qy 789 AATTGGGACTGGCTTACAGTTTCGGAGCTTTGTCATGATTTGTCATGATCTGCTGC 908
Db 56881 AATTGGGCTGGCTTACAGTTTCAGAGATTTCAGTCCATTATCATCATCGTAGGAAGTATG 56940

Qy 849 GCAGCATTAAGCAGACATGATGTTGGAGAGGAGCTGAGATTTCTGATCTGATCTGC 908
Db 56941 GTAGCATCCAGGCGAGACATGGTGTGGACAAAGGGGCTTAAGAGTTCTATATCTTGATCCAT 57000

Qy 909 AAGCAATAAAGGAGACTGTGTGCGACACTATACACAGCTTGAACATAGGAGACTCAAA 968
Db 57001 AGGACGACAGAGGGGACTGTATACCACTGGGTGTAGCTTGACATAGGAGATCTCAA 57060

Qy 969 GCCTGTCCCCCAGTGAACAACTTCCTCCAAAGGTCATACCTCTTAATAATACCAATTT 1028
Db 57061 GCCCAACTCCCAATGACACACTTCCTCCAAAGGCGCACCTCTTAATAGTACCACCTT 57120

Qy 1029 CTTATGAGGCGAGCATTTCAAAACACATGATCTATGAGGGCCAA 1071
Db 57121 CCTGTGGGCCAAGCATTTCAAAACACAGGAGTTTGTGGAGGCCAA 57163

RESULT 15
US-10-942-954-2
; Sequence 2, Application US/10942954
; Publication No. US20050144662A1
; GENERAL INFORMATION:
; APPLICANT: BML, INC.
; APPLICANT: Masataka NAKAMURA
; APPLICANT: Kazuo SUGAMURA
; APPLICANT: Shoichi TAKANO
; APPLICANT: Kinya NAGATA
; APPLICANT: Hiroyuki HIRAI
; TITLE OF INVENTION: KNOCKOUT MOUSE
; FILE REFERENCE: Q83632
; CURRENT APPLICATION NUMBER: US/10/942,954
; CURRENT FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: JP 2003-328480
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 16940
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; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (6)...(6)
; OTHER INFORMATION: n is a, c, g, or t
US-10-942-954-2

Query Match 12.0%; Score 186; DB 22; Length 16940;
Best Local Similarity 76.3%; Pred. No. 8e-40;
Matches 255; Conservative 0; Mismatches 75; Indels 4; Gaps 2;

Qy 750 GAGATCCAGACTAAGACAACTCTAATAAGGGAACATTTAATTGGGACTGGCTTACAGTT 809
Db 2767 GACACCATGACCTGGGTAATTTTCATAAAGAAACATTTAATTGGTACTGGCTTACAGTT 2826

Qy 810 TCGGAGCTTTTGTCCATGATTATCATAGTGGGAAGCATGGCAGCATCTAAGCAGACATGA 869
Db 2827 TCAGAGGTCTAGTCCATTATTGCCATGTTAGGA--CATAGTGGCATGCAGGCAGACAGA 2884

Qy 870 TGTGGAGAGGAGCTGAGATTTCTGCATCTTGCATCTTGCATCTGCAAGCAATAAAGGAGACTGTG 929
Db 2885 TGCTGGAGAGGAGCTGAGAGTTTCTACATCTTGATCCAAAGTCAGCAGAAGGAGACTGTG 2944

Qy 930 TGCCACACTATACACAGCTTGAACATAGGAGACTCAAGCCCTGTCCCCACAGTGACAA 989
Db 2945 TGCCACACTGGGTGTAGCTTGAGCATAGGAGACTCAAGCCCTGTCCCCACAGTGACACA 3004

Qy 990 CTTCTCTCCAAAGGTCATACCTCTTAATAATACCAT--TTCTTATGAGGCAAGCATTTCA 1047
Db 3005 TTTCTCTCCAAAGGCGCATACCTACTACTAGTGTCTACTCTCTATGGGTCAAGCATTTCA 3064

Qy 1048 AACACATGATCTATGAGGCGCCAAACCAATTTCAA 1081
Db 3065 AACACTTGATCTATGGGGTCATTTCTCTTTTAA 3098
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Search completed: September 9, 2005, 08:34:38  
Job time : 3525.54 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 13:43:46 ; Search time 18110.6 Seconds  
(without alignments)  
3257.733 Million cell updates/sec

Title: US-10-622-407-7  
Perfect score: 1550  
Sequence: 1 ttgcactcgccatgttgg.....aatgcacaaaaaaaaaaaaa 1550

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hic: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1521.8	98.2	4224	3	BC076592 Mus muscu
2	1475.8	95.2	2276	3	AK012838 Mus muscu
3	761.4	49.1	1003	6	BY711952 BY711952
4	752.4	48.5	756	7	CK634366 UI-M-HN0-
5	751.4	48.5	765	7	CN461442 UI-M-HB0-
6	734.2	47.4	784	6	CB723050 UI-M-GH0-
7	708	45.7	708	6	CB525851 UI-M-PY0-
8	694.4	44.8	696	5	BU611594 UI-M-PI0-
9	670.4	43.3	683	7	CF729486 UI-M-HD0-
10	539.2	34.8	552	2	AW544660 C0184C12-
11	505.4	32.6	863	6	CB587413 AGENCOURT
12	460.4	29.7	480	4	BI788944 i64le08.Y
13	454.8	29.3	614	7	CN687949 E0250A07-
14	448.2	28.9	639	4	BG077775 H3019F06-
15	438.8	28.3	458	5	BQ033912 UI-1-CF0-
16	434.2	28.0	447	2	AW538894 C0113808-
17	428.4	27.6	438	1	AA182278 mt76f09.f
18	416.2	26.9	437	5	BQ031584 UI-1-CF0-
19	407.8	26.3	411	1	AA754807 v021f11.f
20	404	26.1	410	9	CG651536 OST412784
21	392	25.3	415	9	CG535649 OST122794
22	380	24.5	597	7	CN697902 E0401A05-
23	369.6	23.8	489	7	CK333918 H8266D02-
24	364	23.5	585	2	BB613091 BB613091

25	362.2	23.4	375	6	BY527094
26	362	23.4	487	6	CA879822 AG978B09-
27	362	23.4	942	4	BG918267 B02818449
28	342.4	22.1	430	8	BB784219 BB784219
29	342	22.1	469	8	AQ978007 RPCI-23-3
30	316.4	20.4	371	5	BY182663 BY182663
31	304.2	19.6	331	5	BY343934 BY343934
32	301	19.4	351	5	BY208766 BY208766
33	295	19.0	317	5	BY345556 BY345556
34	290	18.7	438	7	CN692087 E0318B06-
35	284.6	18.4	338	7	CF578223 AGENCOURT
36	278.4	18.0	410	5	BY183172 BY183172
37	266.4	17.2	331	5	BY195969 BY195969
38	233.4	15.1	346	5	BY010018 BY010018
39	232.8	15.0	347	5	BB873121 BB873121
40	229.4	14.8	341	5	BY036522 BY036522
41	228	14.7	544	1	AI747041 u112901.Y
42	223	14.4	338	5	BY325940 BY325940
43	221.8	14.3	297	2	BE381534 B01272537
44	220.8	14.2	755	8	AZ836976 2M0132M06
45	216.6	14.0	629	8	AZ583966 1M0388L12

## ALIGNMENTS

RESULT 1	BC076592	4224 bp	mRNA	linear	HTC 27-JUL-2004
LOCUS	BC076592				
DEFINITION	Mus musculus tumor necrosis factor receptor superfamily, member 22, mRNA (cDNA clone IMAGE:30652769).				
ACCESSION	BC076592				
VERSION	BC076592.1	GI:50370338			
KEYWORDS	HTC.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	1 (bases 1 to 4224)				
AUTHORS	Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Haieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Donald, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullahy, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalob, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Madan, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butlerfield, Y.S., Krzywinski, M.I., Skalska, U., Smalios, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.				
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A.	99 (26)	16899-16903	(2002)	
PUBMED	12477932				
REFERENCE	2 (bases 1 to 4224)				
AUTHORS	Strausberg, R.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-JUL-2004) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA				
REMARK	NIH-MGC Project URL: <a href="http://mgc.nci.nih.gov">http://mgc.nci.nih.gov</a>				
COMMENT	Contact: MGC help desk Email: <a href="mailto:cgapbs-r@mail.nih.gov">cgapbs-r@mail.nih.gov</a> Tissue Procurement: Dr. Jim Lin, University of Iowa cDNA Library Preparation: M. Bento Soares, University of Iowa				







Qy	561	GAGTGTGCTAATTGTCCTCGTTGTTGTTCTTCGGTATCATAGAAGATAAAGGTTCTTACAG	620
Db	602	GAGTGTGCTAATTGTCCTCGTTGTTGTTCTTCGGTATCATAGAAGATAAAGGTTCTTACAG	661
Qy	621	ATGTTTTTCTTAGCTTCTTTTATTTATTTGCTATGAAGTGATCTATGAGGCAACTCTTTTATT	680
Db	662	ATGTTTTTCTTAGCTTCTTTTATTTGCTATGAAGTGATCTATGAGGCAACTCTTTTATT	721
Qy	681	TTATTTATTTTATTTTATTTTATTTTAAATGTTCTTGAACTTGATTTGAAGCCAGGCTGGCCTC	740
Db	722	TTATTTATTTTATTTTATTTTATTTTAAATGTTCTTGAACTTGATTTGAAGCCAGGCTGGCCTC	781
Qy	741	AAATTCACAGAGATCCAGACTAAGACAACTCTATATAGGGAACAATTAAATGGGACTGG	800
Db	782	AAATTCACAGAGATCCAGACTAAGACAACTCTATATAGGGAACAATTAAATGGGACTGG	841
Qy	801	CTTACAGTTTCGGAGCTTTCTGTCATGATTTATCATAGTGGGAAGCATGGCAGCATCTAAG	860
Db	842	CTTACAGTTTCGGAGCTTTCTGTCATGATTTATCATAGTGGGAAGCATGGCAGCATCTAAG	901
Qy	861	CAGACATGATGTTGGAGAGGAGCTGAGATTTCTGCACTCTTGATCTGCAAGCAATAAAG	920
Db	902	CAGACATGATGTTGGAGAGGAGCTGAGATTTCTGCACTCTTGATCTGCAAGCAATAAAG	961
Qy	921	GAGACTGTGTCACACTATACACAGCTTGGAACATAGAGACCTCAAGCCTGTCCCCAC	980
Db	962	GAGACTGTGTCACACTATACACAGCTTGGAACATAGAGACCTCAAGCCTGTCCCCAC	1021
Qy	981	AGTGACAACTTCTCTCAACAAAGGTCATCTCTCTAATAATACCATTTCTTTATCAGGCAA	1040
Db	1022	AGTGACAACTTCTCTCAACAAAGGTCATCTCTCTAATAATACCATTTCTTTATCAGGCAA	1081
Qy	1041	GCATTCAACACATGAGTCTATGAGGGCCAAACCAATTTCAAACCAACACAGGTTAAACAT	1100
Db	1082	GCATTCAACACATGAGTCTATGAGGGCCAAACCAATTTCAAACCAACACAGGTTAAACAT	1141
Qy	1101	TGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCTCTGAGAGTAAGTAACAAATTTAGATGAAG	1160
Db	1142	TGCCCTCTGCAGCTCTCTGGTGGAGGCCCTCTCTGAGAGTAAGTAACAAATTTAGATGAAG	1201
Qy	1161	GCAAGTCTCTGTTATCAGGTCCAAAGAACTCAGATGAATGGTCCACTGTGGTTCTCTAT	1220
Db	1202	GCAAGTCTCTGTTATCAGGTCCAAAGAACTCAGATGAATGGTCCACTGTGGTTCTCTAT	1261
Qy	1221	TAAACATCTGAAGAACATGACCTCACCTTACACGCTCTCCACCTCACTGACTTCCCTTCCC	1280
Db	1262	TAAACATCTGAAGAACATGACCTCACCTTACACGCTCTCCACCTCACTGACTTCCCTTCCC	1321
Qy	1281	CTAGCTTCTCATTTCCAGGTAACCTGCGCATTTTGTGTAATGTGCTTCTTGTCTTCTTC	1340
Db	1322	CTAGCTTCTCATTTCCAGGTAACCTGCGCATTTTGTGTAATGTGCTTCTTGTCTTCTTC	1381
Qy	1341	CTCTCTTTTCCCTCTCTCTCTGGTCCCTTACTTCTCTTCTCTCCACTCTCCACCGCC	1400
Db	1382	CTCTCTTTTCCCTCTCTCTCTGGTCCCTTACTTCTCTTCTCTCCACTCTCCACCGCC	1441
Qy	1401	TCCTCTTAAGCCCTGAATCAGTCTGTAGGTCATGTTTAAATCTACTACTTTCTCTCTGCTC	1460
Db	1442	TCCTCTTAAGCCCTGAATCAGTCTGTAGGTCATGTTTAAATCTACTACTTTCTCTCTGCTC	1501
Qy	1461	TGGACTCATCAGATGCTCTGGCTGAGCTCTCCCTCTCTATCTACATAAACCCTTCCC	1520
Db	1502	TGGACTCATCAGATGCTCTGGCTGAGCTCTCCCTCTCTATCTCAATATAAACCCTTCCC	1561
Qy	1521	CCTAACAGAAATGCAAAA	1539
Db	1562	CCTAACAGAAATGGAACA	1580

RESULT 3  
BY711952  
LOCUS BY711952  
DEFINITION RIKEN full-length enriched, 10, 11 days embryo whole body  
1003 bp mRNA linear EST 16-DEC-2002

ACCESSION	BY711952
VERSION	GI:27123215
KEYWORDS	EST.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1003)
AUTHORS	Nikaido, I., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schombach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C., Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuoka, H., Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brust, V., Chothia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T., Gariboldi, M., Glissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Kongaya, A., Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G., Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S., Ravasi, T., Read, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M., Sandelin, A., Schneider, C., Sempie, C.A., Setou, M., Shimada, K., Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M., Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y., Wells, C., Wilming, L.G., Wynshaw-Boris, A., Yanagisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S., Rogers, J., Birney, E. and Hayashizaki, Y.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
MEDLINE	22354683
PUBMED	12466851
COMMENT	Contact: Yoshihide Hayashizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Teurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/ Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hashizume, W., Hayashida, K., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Koya, S., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Saito, R., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Takeda, Y., Waki, K., Watahiki, A., Muramatsu, M. and Hayashizaki, Y. Direct Submission Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001) Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000) RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000) Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001) cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.

## FEATURES

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/clone="2810028K06"
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## ORIGIN

[illegible]

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Db	840	ACAGTTTTCGACGTTTTTGTCCATGATTATCATATAGTGGG-AGCATGGCAGCATCTA	893
RESULT 4			
LOCUS	CK634366	756 bp	mRNA
DEFINITION	UI-M-HN0-cn1-e-07-0-UI.r1 N1H_BMAP_HN0 Mus musculus CDNA clone	linear	EST 28-JAN-2004
ACCESSION	CK634366		
KEYWORDS	CK634366.1	GI:41360232	
SOURCE	EST.		
ORGANISM	Mus musculus		
	Mus musculus		
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;		
REFERENCE	1 (bases 1 to 756)		
AUTHORS	N1H-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Robert Strausberg, ph.D.		

COMMENT

Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Dr. James Lin University of Iowa  
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa  
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa  
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa  
Clone Distribution: Distribution information can be found at  
<http://genome.uiowa.edu/distribution/mousefl.html>  
This clone was contributed by the Brain Molecular Anatomy Project  
(BMAP)

The following repetitive elements were found in this cDNA  
(cont.)  
sequence: 119-146, >(TAAAA)#simple\_repeat (matched complement)  
151-201, >B1 MW#SINE/Alu (matched complement) 194-535,  
>ORR1B#LTR/MaLR (matched complement)  
Seq primer: pYX-5.

**FEATURES**  
**SOURCE**

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/lab_host="DH10B (T1 phage resistant)"
/clone_lib="NIH_BMAP_RNO"
/notes="Organ: Head; Vector: pYX-Asc; Site1: EcoR I; Site2: Not I; The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. Denatured RNA was size fractionated on a 1% agarose gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is CGAAGTCAAT. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH)."

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## ORIGIN

Query Match	Score	DB	Length
Best Local Similarity	99.6%	Pred. No. 5.6e-175	Length 756
Matches 753; Conservative	0;	Mismatches 3;	Indels 0; Gaps 0;

  

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Qy 676 TTTATTTTATTTTATTTTATTTTATTTTAAATGCTCTTGAACCTTGATTTTGAAGCAGGCTG 735
Db |||||||
Qy 121 TTTATTTTATTTTATTTTATTTTATTTTAAATGCTCTTGAACCTTGATTTTGAAGCAGGCTG 180
Db |||||||
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Db |||||||
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Qy 241 ACTGCTTACAGTTTCGAGCTTTTGTCCATGATTATCATAGTGGAGAGCATGCGCAT 300
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Db |||||||
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Qy 916 AAAAGGAGACTGTGTGCCACACTATACACAGCTTGAACATGAGGAGCTTCAAGCCTGTC 975
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LOCUS
DEFINITION
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  UI-M-HB0-coy-c-18-0-UI.r1 NIH BMAP_HB0 Mus musculus cDNA clone
  IMAGE:30652769 5', mRNA sequence.
ACCESSION
  CN461442
VERSION
  CN461442.1 GI:46467168
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  (bases 1 to 765)
REFERENCE
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: csapbs-remail.nih.gov
  Tissue Procurement: Dr. James Lin University of Iowa
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Distribution information can be found at
  http://genome.uiowa.edu/distribution/mousefl.html
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This clone was contributed by the Brain Molecular Anatomy Project (BMAP).  
The following repetitive elements were found in this cDNA  
sequence: 75-111, >(CAG)n#Simple repeat (matched complement)  
683-710, >(TAAAA)n#Simple repeat (matched complement) 715-765,  
>BL MM#SINE/Alu (matched complement)  
Seq primer: pYX-5

#### FEATURES

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Site 2: Not I; The library was constructed according  
Bonaldi, Lennon and Soares, Genome Research, 6:791-806,  
1996. Denatured RNA was size fractionated on a 1% agarose  
gel. First strand cDNA synthesis was primed with oligo-dT  
primer containing a Not I site. Double strand cDNA was  
size selected according to mRNA size fraction. Ligated  
with EcoR I adaptor, digested with NotI and then cloned  
directionally into pYX-Asc vector. The library tag  
sequence located between the Not I site and the polyA tail  
is TTTATGTAAGT. This library was created for the University  
Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the  
Developing Mouse Nervous System', supported by National  
Institute of Mental Health (NIMH)."

#### ORIGIN

Query Match 48.5%; Score 751.4; DB 7; Length 765;  
Best Local Similarity 99.5%; Pred. No. 9.9e-175;  
Matches 752; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
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Db |||||||  
Qy 10 TTGCACCTCGGCCATGTTTGGCTTCTTCTGCAGCTTGGTGCAGTCTGAGTCTGGTTC 69  
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KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 708)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 35-71, >(CAG)n#simple_repeat (matched complement)
643-670, >(TAAAA)n#simple_repeat (matched complement)
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Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is AGCAGACAG. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH), Hemin Chin, Ph.D.,
program coordinator."
ORIGIN
Query Match 45.7%; Score 708; DB 6; Length 708;
Best Local Similarity 100.0%; Pred.No. 5.4e-164;
Matches 708; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 TGCTGCTGCTGAATCTGCGCCCTTGCGAGGTAAATTTGCTATGCTAGAAATTACACTCTTCA 120
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ACCESSION BU611594
VERSION BU611594.1 GI:23277809
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 696)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)
The following repetitive elements were found in this cDNA
sequence: 35-75, >(CAG)n#simple_repeat (matched complement)
647-674, >(TAAAA)n#simple_repeat (matched complement)
Seq primer: pYX-5.
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
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/db_xref="taxon:10090"
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/tissue_type="whole brain"
/dev_stage="embryo 12.5dpc"
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Db 600 AGTGATCTATGGAGGCAACTCTTTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 659
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## RESULT 10

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DEFINITION musculus cDNA clone C0184C12 3', mRNA sequence.
ACCESSION AW544660
VERSION AW544660.1 GI:7187077
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 552)
Tanaka,T.S., Jaradat,S.A., Lim,M.K., Kargul,G.J., Wang,X.,
Grahovac,M.J., Pantano,S., Sano,Y., Piao,Y., Nagaraja,R., Doi,H.,
Wood,W.H. III, Becker,K.G. and Ko,M.S.H.
Genome-wide expression profiling of mid-gestation placenta and
embryo using a 15,000 mouse developmental cDNA microarray
Proc. Natl. Acad. Sci. U.S.A. 97 (16), 9127-9132 (2000)
20381348
10922068
Contact: George J. Kargul
Laboratory of Genetics
National Institute on Aging/National Institutes of Health
333 Cassell Drive, Suite 4000, Baltimore, MD 21224-6820, USA
Email: cdna@igsun.grc.nia.nih.gov
Plate: C0184 row: C column: 12
Seq primer: -21M13 Forward
High quality sequence stop: 552
POLYA=yes.

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## FEATURES

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source
Location/Qualifiers
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/lab_host="DH10B"
/clone_lib="NIA Mouse E7.5 Extraembryonic Portion cDNA
Library"
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Site 1: SalI; Site 2: NotI; Total RNAs were extracted from
5 EPC. The double-stranded cDNA was synthesized by
Gibco's kit with an Oligo(dT) primer [NotI primer-adaptor
from GibcoBRL]
[5'-pGACTAGTCTAGATCGAGGCGCGCTTTTCTTTTCTTTT-3']
from 0.8ug of mRNA. The double-stranded cDNAs were
treated with T4 DNA polymerase and purified by
ethanol-precipitation. The cDNAs were ligated to
EcoRI-linker l3-Sal3 (include SalI sequence). The cDNAs
were purified by phenol/chloroform and separated from
free linkers by Centricon 100. Then, cDNAs were amplified
by long-range high fidelity PCR using Takara's Ex Taq
polymerase. Then, the cDNAs were purified by
phenol/chloroform and by Centricon 100. The cDNAs were
digested with SalI and NotI enzymes. Then, the cDNAs were
size selected by Gibco's Size Fractionation Column. The
cDNAs were cloned into SalI/NotI site of pSPORT1 plasmid
vector. The DH10B E. coli host was transformed with the
ligation mixture by chemical method. The library was
constructed by Xiaohong Wang."

```

## ORIGIN

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Query Match 34.8%; Score 539.2; DB 2; Length 552;
Best Local Similarity 98.6%; Pred. No. 3.le-122;
Matches 544; Conservative 0; Mismatches 8; Indels 0; Gaps 0;
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Db 552 CACAGTCACAACTTCCTCCAAACAGGTCTACCTCTTAATATACCATTTCTTTATGAGG 493
Qy 1038 CAACGATTTCAAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACACCAAGTTAAC 1097
Db 492 CAACGATTTCAAAACACATGAGTCTATGAGGGCCAAACCAATTCAAACACCAAGTTAAC 433
Qy 1098 AATTGCCCTCTGAGCTCTCTGTTGAGGGCCCTCTTGTAGAGTGAAGTAACAAATTTAGATG 1157
Db 432 AATTGCCCTCTGAGCTCTCTGTTGAGGGCCCTCTTGTAGAGTGAAGTAACAAATTTAGATG 373
Qy 1158 AAGCAAGTCTCTGTTATCAGGTCCAAAGAAACCTCAGATGAAATGGTCCACTGTGGTTCC 1217
Db 372 AAGCAAGTCTCTGTTATCAGGTCCAAAGAAACCTCAGATGAAATGGTCCACTGTGGTTCC 313
Qy 1218 TATTAACATATCTGAAGAACATGACCTCACCTTACACGTTCCACCTCACTGACCTTCCTT 1277
Db 312 TATTAACATATCTGAAGAACATGACCTCACCTTACACGTTCCACCTCACTGACCTTCCTT 253
Qy 1278 CCCCTAGTTCTCATTTCCAGGTAAACCTGCCATTTTGTGATATGTGCTTCTTGGTTC 1337
Db 252 CCCCTAGTTCTCATTTCCAGGTAAACCTGCCATTTTGTGATATGTGCTTCTTGGTTC 193
Qy 1338 TTCTCTCTCTTTCCCTCTCTCTCTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1397
Db 192 TTCTCTCTCTTTCCCTCTCTCTCTGTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 133
Qy 1398 GCCTCTCTTTAAGGCCCTGAATCAGTCTGTAGGTGATGTTTAAATCTATCTATTTCTCTG 1457
Db 132 GCCTCTCTTTAAGGCCCTGAGTCTGTAGGTGATGTTTAAATCTATCTATTTCTCTCTG 73
Qy 1458 CTCTGGACTCATCCAGATGTTCTCTGGCTGAGCTCTCCCTCTCTCTCTCTCTCTCTCTCT 1517
Db 72 CTCTGGACTCATCCAGATGTTCTCTGGCTGAGCTCTCCCTCTCTCTCTCTCTCTCTCTCT 13
Qy 1518 CCCCCTAACCCAG 1529
Db 12 CCCCCTAACCCAG 1

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RESULT 11  
CB587413

LOCUS CB587413 863 bp mRNA linear EST 03-APR-2003  
 DEFINITION AGNCOURT\_12970406 NIH MGC\_136 Mus musculus cDNA clone  
 IMAGE:30294625 5', mRNA sequence.  
 ACCESSION CB587413  
 VERSION CB587413.1 GI:29505269  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgi.nci.nih.gov/.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Dr. David Rowe  
 CDNA Library Preparation: Invitrogen Corp  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov  
 Plate: NDA342 row: a column: 02  
 High quality sequence stop: 550.  
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 Location/Qualifiers  
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 /mol\_type="mRNA"  
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 /tissue\_type="embryonic limb, maxilla and mandible"  
 /lab\_host="DH10B (phage-resistant)"  
 /clone\_lib="NIH MGC 136"  
 /note="Vector: pCMV-SPORT6.1; Site 1: EcoRV, Site 2: NotI; Normalized, full-length enriched library from pool of mouse embryonic limb, maxilla and mandible, embryonic day 17.5, 18.5 and newborn (mandible (5, 4 and 1 limb and jaw equivalents from respective days). Cloned directionally, oligo-dr primed (5'-GACTAGTCTAGATCGCGCGCCGCTT)15-3'. Size selected for the 1kb fragments, average insert size 1.2 kb. Normalization to Cot 7.5. Tissue contributed by David Rowe; library constructed by ResGen, Invitrogen Corp. Note: this is a NIH\_MGC Library."  
 ORIGIN  
 Query Match 32.6%; Score 505.4; DB 6; Length 863;  
 Best Local Similarity 97.9%; Pred. No. 7.8e-114;  
 Matches 512; Conservative 0; Mismatches 11; Indels 0; Gaps 0;  
 1028 TCTTATGAGGCAAGCATTCAACACATGAGTCTATGAGGCGCAACCAATTCAAACACC 1087  
 Db 1 TCTTATGAGGCAAGCATTCAACACATGAGTCTATGAGGCGCAACCAATTCAAACACC 60  
 1088 ACAGTTTAACTTGCCTCTGAGCTCTCTGGTGGAGGCGCTCTTGGAGAGTAAGTAAC 1147  
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 1148 AATTAGATGAAGCAAGTCTCTGTATCAGTCTCAAGAAAGAACTCAGATGAATGTCCA 1207  
 Db 121 AATTAGATGAAGCAAGTCTCTGTATCAGTCTCAAGAAAGAACTCAGATGAATGTCCA 180  
 1208 CTGTGGTTCCTATTAACTACTGAAGAACATGACCTCACCTTACACGCTCTCCACCTCACT 1267  
 Db 181 CTGTGGTTCCTATTAACTACTGAAGAACATGACCTCACCTTAGACTTCTCCACCTCACT 240  
 1268 GACTTCCCTTCCCTAGTCTTCAATTCACAGTAACCCCTGCGCAATTTTGGTAATGTGCC 1327  
 Db 241 GGCTTCCCTTCCCTAGTCTTCAATTCACAGTAACCCCTGCGCAATTTTGGTAATGTGCC 300  
 1328 TTCTTGGTTCCTCTCTCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1387  
 Db 301 TTCTTGGTTCCTCTCTCTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360

Qy 1388 CTCTCCACCGAGCTCTCTTAAAGGCTGAATCAGTCTGTAGGTCATGTTTAACTACTAC 1447  
 Db 361 CTCTCCACCGAGCTCTCTTAAAGGCTGAATCAGTCTGTAGGTCATGTTTAACTACTAC 420  
 Qy 1448 TTTCTCTCTGCTCTGGACTCATCCAGATGCTCTGGCTGAGCTCTCCCTCTATCTACAA 1507  
 Db 421 TTTCTCTCTGCTCTGGACTCATCCAGATGCTCTGGCTGAGCTCTCCCTCTATCTACAA 480  
 Qy 1508 TAAACCCCTTCCCTAAACAGAAATGCAAAAAA 1550  
 Db 481 TAAACCCCTTCCCTAAACAGAAATGCAAAAAA 523  
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 ACCESSION BI788944  
 VERSION BI788944.1 GI:15816669  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 480)  
 REFERENCE  
 AUTHORS  
 Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blustein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvili, R., Williams, T., Jackson, Y. and Bowers, Y.  
 Endocrine Pancreas Consortium  
 Unpublished (2000)  
 TITLE  
 JOURNAL  
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue  
 Endocrine Pancreas Consortium  
 Harvard University, Howard Hughes Medical Institute  
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138  
 Tel: 617-495-1812  
 Fax: 617-495-8557  
 Email: dmelton@biohp.harvard.edu  
 Pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000) Library was constructed by Catherine Lee DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Marie Searce (msearce@mail.med.upenn.edu)  
 Seq primer: -40RP from Gibco  
 High quality sequence stop: 429.  
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 /clone\_lib="Kaestner ngn3 wt"  
 /notes="Organ: pancreas; Vector: pSPORT1 (GIBCO); Site\_1: Not I; Site\_2: Sal I; The library was prepared by Catherine S. Lee and has not been published. The pancreas was obtained from Gerard Gradwohl (PNAS 97 P1607-1611, 2000). The cDNA's were prepared with an oligo containing a NotI site, and SalI linkers were added to the ends. The inserts were cut with NotI before being cloned into the NotI-SalI sites in the vectors. This is one of two libraries, ngn3 wt and ngn3 -/- . The wt library is in pSPORT1, T7 promoter is 5'."  
 ORIGIN  
 Query Match 29.7%; Score 460.4; DB 4; Length 480;  
 Best Local Similarity 99.8%; Pred. No. 9.5e-103;  
 Matches 461; Conservative 0; Mismatches 1; Indels 0; Gaps 0;







GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 8, 2005, 17:05:32 ; Search time 598.714 Seconds  
(without alignments)  
127.905 Million cell updates/sec

Title: US-10-622-407-8  
Perfect score: 1087  
Sequence: 1 MFGFFCSLSSLRFLWR.....LLSPLSVLVVVVFRIIR 198

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseqp1980s:\*  
2: Geneseqp1990s:\*  
3: Geneseqp2000s:\*  
4: Geneseqp2001s:\*  
5: Geneseqp2002s:\*  
6: Geneseqp2003as:\*  
7: Geneseqp2003bs:\*  
8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1087	100.0	198	7	Abw02715 Mouse tms
2	1087	100.0	198	8	Adj45752 Murine tm
3	962	88.5	398	7	Abw02717 Mouse tms
4	962	88.5	398	8	Adj45758 Murine tm
5	956	87.9	180	7	Abw02716 Mouse tms
6	956	87.9	180	8	Adj45754 Murine tm
7	748	68.8	133	7	Abw02714 Mouse tms
8	748	68.8	133	8	Adj45750 Murine tm
9	746.5	68.7	176	2	AAW80254 Amino aci
10	746.5	68.7	176	8	Adf57551 Mouse ymk
11	746.5	68.7	176	8	Adm46623 Mouse 7F4
12	711	65.4	396	8	Adf57557 Mouse ymk
13	682.5	62.8	148	8	Adm46624 Mouse 7F4
14	542.5	49.9	380	4	Abg09344 Novel hum
15	467	43.0	117	8	Adf57549 Mouse ymk
16	320	29.4	204	5	Abb81467 Murine TA
17	226	20.8	247	8	Adf57553 Mouse TNF
18	226	20.8	454	5	Aao22289 TNFRI exp
19	226	20.8	454	8	Adt08167 Murine tu
20	218.5	20.1	242	8	Adf57552 Mouse Fas
21	218.5	20.1	327	2	AAR41688 Murine Fa
22	218.5	20.1	327	2	AAR78611 Murine Fa
23	218.5	20.1	327	2	AAR2530 mFas sequ
24	218.5	20.1	327	2	AAW86241 Fas ligan
25	218.5	20.1	327	3	AAB19344 Amino aci

26	218.5	20.1	327	8	ADL27705	Adl27705	Mouse Fas
27	218.5	20.1	327	8	ADM53477	Adm53477	Mouse Fas
28	212.5	19.5	461	7	ADE57927	Ade57927	Rat Prote
29	212.5	19.5	461	8	ADQ76809	Adq76809	Rat solub
30	211.5	19.5	461	2	ABG74754	Abg74754	Rat TNF-R
31	211.5	19.5	461	2	AAR07450	Aar07450	Rat Tumou
32	208.5	19.2	355	2	AAR85073	Aar85073	Cowpox vi
33	208.5	19.2	355	4	AAB50524	Aab50524	Human tum
34	208.5	19.2	355	8	ADJ96165	Adj96165	Human CRM
35	207.5	19.1	285	2	AAW33359	Aaw33359	TBP(20-19
36	205	18.9	350	5	ABB81468	Abb81468	Viral Crm
37	203.5	18.7	256	2	AAW33357	Aaw33357	TBP(20-16
38	203.5	18.7	307	2	AAW33358	Aaw33358	TBP(20-16
39	203.5	18.7	336	2	AAW33360	Aaw33360	TBP(20-19
40	203.5	18.7	884	2	AAR70109	Aar70109	TNF-R-GBP
41	202.5	18.6	658	5	AAW49759	Aam49759	TNF-selec
42	201.5	18.5	168	2	AAR24084	Aar24084	Truncated
43	201.5	18.5	197	6	ADA49707	Ada49707	Extracell
44	201.5	18.5	199	2	AAR24080	Aar24080	Truncated
45	201.5	18.5	211	2	AAW89225	Aaw89225	Tumour ne

ALIGNMENTS

RESULT 1		ABW02715	
ID	ABW02715	standard; protein; 198 AA.	
XX	AC	ABW02715;	
XX	DT	11-MAR-2004 (first entry)	
XX	DE	Mouse tmst2-receptor protein.	
XX	KW	Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;	
KW	KW	cachexia; autoimmune disease; inflammatory disease; chromosome mapping;	
KW	KW	cancer; chromosome identification; gene therapy; antibacterial; virucide;	
KW	KW	immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;	
KW	KW	cytostatic; mouse.	
XX	OS	Mus musculus.	
XX	PN	US6627199-B1.	
XX	PD	30-SEP-2003.	
XX	PF	07-JUL-2000; 2000US-00612033.	
XX	PR	09-JUL-1999; 99US-0143063P.	
XX	PA	(AMGE-) AMGEN INC.	
XX	PI	Saris C;	
XX	DR	WPI; 2003-874309/81.	
DR	DR	N-PSDB; AAD64754.	
XX	PT	New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,	
PT	PT	treating or ameliorating diseases associated with or resulting from for	
PT	PT	abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for	
XX	XX	chromosome mapping.	
PS	PS	Claim 1; SEQ ID NO 8; Opp; English.	
XX	CC	The invention relates to transmembrane decoy-receptor (tmst2) proteins	
CC	CC	and their secreted splice variants, belonging to the tumour necrosis	
CC	CC	factor (TNF) receptor super gene family and polynucleotides encoding such	
CC	CC	proteins. The composition and methods are useful in diagnosing, treating	
CC	CC	or ameliorating diseases associated with or resulting from abnormal tmst2	
CC	CC	and/or abnormal expression of its putative ligand, such as sepsis,	
CC	CC	cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial	
CC	CC	and parasitic diseases or cancer. They may also be used for chromosome	

CC identification or mapping. The invention is useful in gene therapy. The  
CC present sequence is mouse tmst2-receptor protein used in the  
CC exemplification of the invention  
XX  
XX  
SQ Sequence 198 AA;  
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Best Local Similarity 100.0%; Pred. No. 1e-81;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 61 KNCAGTFVVKAPCEIPHTQGCCEKCHPGTFTEKDYLDACILCSTCDKQEMVADCSATS 120  
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Db 121 DRKCQCRGTGLYYDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFILL 180  
Qy 181 SPLSVLIVSVVVFRIIR 198  
Db 181 SPLSVLIVSVVVFRIIR 198  
RESULT 2  
ADJ45752  
ID ADJ45752 standard; protein; 198 AA.  
XX  
AC ADJ45752;  
XX  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Murine tmst2-receptor.  
XX  
KW Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;  
KW autoimmune disease; cachexia; cancer; cerebral malaria;  
KW diabetes mellitus; disseminated intravascular coagulation;  
KW haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;  
KW lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;  
KW organ rejection; rheumatoid arthritis; septic shock; stroke;  
KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;  
KW receptor.  
XX  
XX  
OS Mus musculus.  
XX  
XX US2004018544-A1.  
XX  
XX 29-JAN-2004.  
XX  
XX 17-JUL-2003; 2003US-00622407.  
XX  
XX 09-JUL-1999; 99US-0143063P.  
XX  
XX 07-JUL-2000; 2000US-00612033.  
XX  
XX (SARI/) SARIS C.  
XX  
XX Saris C;  
XX  
XX WPI; 2004-224390/21.  
XX  
XX N-PSDB; ADJ45751.  
XX  
XX Novel tmst2-receptor polypeptide useful for diagnosing and treating  
XX disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial  
XX infections.  
XX  
XX Claim 13; SEQ ID NO 8; 57pp; English.  
XX  
XX The invention relates to a tmst2-receptor polypeptides and the  
XX polynucleotide encoding them. The sequences of the invention are useful  
CC for treating diseases and conditions including acquired immunodeficiency  
CC

CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral  
CC malaria, diabetes mellitus, disseminated intravascular coagulation,  
CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,  
CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ  
CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory  
CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.  
CC This sequence represents the murine tmst2-receptor polypeptide of the  
CC invention.  
XX  
XX  
SQ Sequence 198 AA;  
Query Match 100.0%; Score 1087; DB 8; Length 198;  
Best Local Similarity 100.0%; Pred. No. 1e-81;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSFKPCPAGEYSKDVCC 60  
Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSFKPCPAGEYSKDVCC 60  
Qy 61 KNCAGTFVVKAPCEIPHTQGCCEKCHPGTFTEKDYLDACILCSTCDKQEMVADCSATS 120  
Db 61 KNCAGTFVVKAPCEIPHTQGCCEKCHPGTFTEKDYLDACILCSTCDKQEMVADCSATS 120  
Qy 121 DRKCQCRGTGLYYDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFILL 180  
Db 121 DRKCQCRGTGLYYDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFILL 180  
Qy 181 SPLSVLIVSVVVFRIIR 198  
Db 181 SPLSVLIVSVVVFRIIR 198  
RESULT 3  
ABW02717  
ID ABW02717 standard; protein; 398 AA.  
XX  
XX  
AC ABW02717;  
XX  
XX 11-MAR-2004 (first entry)  
DT  
XX  
DE Mouse tmst2-receptor-human immunoglobulin Fc region fusion protein.  
XX  
KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;  
KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;  
KW cancer; chromosome identification; gene therapy; antibacterial; virucide;  
KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;  
KW cytostatic; mouse; human; immunoglobulin Fc region; fusion protein.  
XX  
XX Chimeric - Mus musculus.  
XX  
XX Chimeric - Homo sapiens.  
XX  
XX US6627199-B1.  
XX  
XX 30-SEP-2003.  
XX  
XX 07-JUL-2000; 2000US-00612033.  
XX  
XX 09-JUL-1999; 99US-0143063P.  
XX  
XX (AMGE-) AMGEN INC.  
XX  
XX Saris C;  
XX  
XX WPI; 2003-874309/81.  
XX  
XX N-PSDB; AAD64758.  
XX  
XX New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,  
XX treating or ameliorating diseases associated with or resulting from  
XX abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for  
XX chromosome mapping.  
XX  
XX Example 4; SEQ ID NO 14; Opp; English.  
XX  
XX



CC The invention relates to transmembrane decoy-receptor (tmst2) proteins  
 CC and their secreted splice variants, belonging to the tumour necrosis  
 CC factor (TNF) receptor super gene family and polynucleotides encoding such  
 CC proteins. The composition and methods are useful in diagnosing, treating  
 CC or ameliorating diseases associated with or resulting from abnormal tmst2  
 CC and/or abnormal expression of its putative ligand, such as sepsis,  
 CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial  
 CC and parasitic diseases or cancer. They may also be used for chromosome  
 CC identification or mapping. The invention is useful in gene therapy. The  
 CC present sequence is a fusion protein comprising mouse tmst2- receptor  
 CC protein and human immunoglobulin Fc region. This sequence is used in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 398 AA;

Query Match 88.5%; Score 962; DB 7; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-71;  
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 DB 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 QY 61 KNCAGTFVKAPCEIPTHQOQCEKCHPGTFTKXNDYLDACILCSTCDKQEMVADCSATS 120  
 DB 61 KNCAGTFVKAPCEIPTHQOQCEKCHPGTFTKXNDYLDACILCSTCDKQEMVADCSATS 120  
 QY 121 DRKQCRGTGLYYDDPKFPESCRCPTKCPQIGIPVLQECNSTANTVCSSSVSN 171  
 DB 121 DRKQCRGTGLYYDDPKFPESCRCPTKCPQIGIPVLQECNSTANTVCSSSVSN 171

RESULT 4  
 ADJ45758  
 ID ADJ45758 standard; protein; 398 AA.

XX AC ADJ45758;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Murine tmst2-Fc fusion protein.  
 XX DE Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;  
 XX KW autoimmune disease; cachexia; cancer; cerebral malaria;  
 XX KW diabetes mellitus; disseminated intravascular coagulation;  
 XX KW haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;  
 XX KW lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;  
 XX KW organ rejection; rheumatoid arthritis; septic shock; stroke;  
 XX KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;  
 XX KW tmst2-Fc fusion protein; receptor.  
 XX OS Mus musculus.  
 XX OS Synthetic.  
 XX PN US2004018544-A1.  
 XX PD 29-JAN-2004.  
 XX PF 17-JUL-2003; 2003US-00622407.  
 XX PR 09-JUL-1999; 99US-0143063P.  
 XX PR 07-JUL-2000; 2000US-00612033.  
 XX PR (SARI/) SARIS C.  
 XX PA Saris C;  
 XX PI WPI; 2004-224390/21.  
 XX DR N-PSDB; ADJ45757.  
 XX DR Novel tmst2-receptor polypeptide useful for diagnosing and treating  
 XX PT disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial  
 XX PT infections.

XX Example 4; SEQ ID NO 14; 57pp; English.  
 XX The invention relates to a tmst2-receptor polypeptides and the  
 CC polynucleotide encoding them. The sequences of the invention are useful  
 CC for treating diseases and conditions including acquired immunodeficiency  
 CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral  
 CC malaria, diabetes mellitus, disseminated intravascular coagulation,  
 CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,  
 CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ  
 CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory  
 CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.  
 CC This sequence represents a murine tmst2-Fc fusion protein of the  
 CC invention.

SQ Sequence 398 AA;  
 Query Match 88.5%; Score 962; DB 8; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 4.1e-71;  
 Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 DB 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 QY 61 KNCAGTFVKAPCEIPTHQOQCEKCHPGTFTKXNDYLDACILCSTCDKQEMVADCSATS 120  
 DB 61 KNCAGTFVKAPCEIPTHQOQCEKCHPGTFTKXNDYLDACILCSTCDKQEMVADCSATS 120  
 QY 121 DRKQCRGTGLYYDDPKFPESCRCPTKCPQIGIPVLQECNSTANTVCSSSVSN 171  
 DB 121 DRKQCRGTGLYYDDPKFPESCRCPTKCPQIGIPVLQECNSTANTVCSSSVSN 171

RESULT 5  
 ABW02716  
 ID ABW02716 standard; protein; 180 AA.

XX AC ABW02716;  
 XX DT 11-MAR-2004 (first entry)  
 XX DE Mouse tmst2-receptor splice variant protein.  
 XX DE Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;  
 XX KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;  
 XX KW cancer; chromosome identification; gene therapy; antibacterial; virucide;  
 XX KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;  
 XX KW cytostatic; mouse; splice variant.  
 XX OS Mus musculus.  
 XX OS US6627199-B1.  
 XX PN 30-SRP-2003.  
 XX PD 07-JUL-2000; 2000US-00612033.  
 XX PF 09-JUL-1999; 99US-0143063P.  
 XX PR (AMGE-) AMGEN INC.  
 XX PA Saris C;  
 XX PI WPI; 2003-874309/81.  
 XX DR N-PSDB; AAD64755.  
 XX DR New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,  
 XX PT treating or ameliorating diseases associated with or resulting from  
 XX PT abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for  
 XX PT chromosome mapping.  
 XX PS Claim 1; SEQ ID NO 10; 0pp; English.

XX The invention relates to transmembrane decoy-receptor (tmst2) proteins  
CC and their secreted splice variants, belonging to the tumour necrosis  
CC factor (TNF) receptor super gene family and polynucleotides encoding such  
CC proteins. The composition and methods are useful in diagnosing, treating  
CC or ameliorating diseases associated with or resulting from abnormal tmst2  
CC and/or abnormal expression of its putative ligand, such as sepsis,  
CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial  
CC and parasitic diseases or cancer. They may also be used for chromosome  
CC identification or mapping. The invention is useful in gene therapy. The  
CC present sequence is mouse tmst2-receptor splice variant protein used in  
CC the exemplification of the invention  
XX  
XX Sequence 180 AA;

Query Match 87.9%; Score 956; DB 7; Length 180;  
Best Local Similarity 100.0%; Pred. No. 5.7e-71;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFGFCSLSVSLSRWFLWRLRLLLLLLLLLLPLQVRFAMLELHSPKCPAGEYWSKDVC 60  
Db 1 MFGFCSLSVSLSRWFLWRLRLLLLLLLLLLPLQVRFAMLELHSPKCPAGEYWSKDVC 60  
Qy 61 KNCAGTFVKAPCEIPHTQGCCKHPGTFTKDNLYLDACILCSTCDKQEMWADCSATS 120  
Db 61 KNCAGTFVKAPCEIPHTQGCCKHPGTFTKDNLYLDACILCSTCDKQEMWADCSATS 120  
Qy 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGPVQLQECNSTANTVCSSSVS 170  
Db 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGPVQLQECNSTANTVCSSSVS 170

RESULT 6  
ADJ45754  
ID ADJ45754 standard; protein; 180 AA.  
XX  
AC ADJ45754;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE Murine tmst2-receptor splice variant polypeptide.  
XX  
KW Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;  
KW autoimmune disease; cachexia; cancer; cerebral malaria;  
KW diabetes mellitus; disseminated intravascular coagulation;  
KW haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;  
KW lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;  
KW organ rejection; rheumatoid arthritis; septic shock; stroke;  
KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;  
KW tmst2-receptor splice variant; receptor.  
XX  
OS Mus musculus.  
XX  
FN US2004018544-A1.  
XX  
PN 29-JAN-2004.  
XX  
PD 17-JUL-2003; 2003US-00622407.  
XX  
PF 09-JUL-1999; 99US-0143063P.  
XX  
PR 07-JUL-2000; 2000US-00612033.  
XX  
XX (SARI/) SARIS C.  
XX  
XX Saris C;  
XX  
XX WPI; 2004-224390/21.  
XX  
DR N-PSDB; ADJ45753.  
XX  
XX Novel tmst2-receptor polypeptide useful for diagnosing and treating  
XX disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial  
XX infections.  
XX

PS Claim 13; SEQ ID NO 10; 57pp; English.  
XX  
CC The invention relates to a tmst2-receptor polypeptides and the  
CC polynucleotide encoding them. The sequences of the invention are useful  
CC for treating diseases and conditions including acquired immunodeficiency  
CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral  
CC malaria, diabetes mellitus, disseminated intravascular coagulation,  
CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,  
CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ  
CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory  
CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.  
CC This sequence represents a murine tmst2-receptor splice variant  
CC polypeptide of the invention.  
XX  
XX Sequence 180 AA;

Query Match 87.9%; Score 956; DB 8; Length 180;  
Best Local Similarity 100.0%; Pred. No. 5.7e-71;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFGFCSLSVSLSRWFLWRLRLLLLLLLLLLPLQVRFAMLELHSPKCPAGEYWSKDVC 60  
Db 1 MFGFCSLSVSLSRWFLWRLRLLLLLLLLLLPLQVRFAMLELHSPKCPAGEYWSKDVC 60  
Qy 61 KNCAGTFVKAPCEIPHTQGCCKHPGTFTKDNLYLDACILCSTCDKQEMWADCSATS 120  
Db 61 KNCAGTFVKAPCEIPHTQGCCKHPGTFTKDNLYLDACILCSTCDKQEMWADCSATS 120  
Qy 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGPVQLQECNSTANTVCSSSVS 170  
Db 121 DRKQCRTGLYYDPKFPESCRCPTKCPQGPVQLQECNSTANTVCSSSVS 170

RESULT 7  
ABW02714  
ID ABW02714 standard; protein; 133 AA.  
XX  
XX AC ABW02714;  
XX  
DT 11-MAR-2004 (first entry)  
XX  
DE Mouse tmst2-receptor protein from tmst2-00004-d1 clone.  
XX  
KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;  
KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;  
KW cancer; chromosome identification; gene therapy; antibacterial; virucide;  
KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;  
KW cytosstatic; mouse.  
XX  
OS Mus musculus.  
XX  
FN US6627199-B1.  
XX  
PN 30-SEP-2003.  
XX  
PD 07-JUL-2000; 2000US-00612033.  
XX  
PF 09-JUL-1999; 99US-0143063P.  
XX  
PR (AMGE-) AMGEN INC.  
XX  
XX Saris C;  
XX  
XX WPI; 2003-874309/81.  
XX  
DR N-PSDB; AAD64753.  
XX  
XX New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,  
XX treating or ameliorating diseases associated with or resulting from  
XX abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for  
XX chromosome mapping.  
XX  
XX Example 1; SEQ ID NO 6; Opp; English.  
XX

CC The invention relates to transmembrane decoy-receptor (tmst2) proteins  
 CC and their secreted splice variants, belonging to the tumour necrosis  
 CC factor (TNF) receptor super gene family and polynucleotides encoding such  
 CC proteins. The composition and methods are useful in diagnosing, treating  
 CC or ameliorating diseases associated with or resulting from abnormal tmst2  
 CC and/or abnormal expression of its putative ligand, such as sepsis,  
 CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial  
 CC and parasitic diseases or cancer. They may also be used for chromosome  
 CC identification or mapping. The invention is useful in gene therapy. The  
 CC present sequence is mouse tmst2-receptor protein used in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 133 AA;

Query Match 68.8%; Score 748; DB 7; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-54;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 DB 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 QY 61 KNCAGTFVKAPCEIPHTQOCEKCHPGTFTKDNLYDACLILCSTCDKQDMVADCSATS 120  
 DB 61 KNCAGTFVKAPCEIPHTQOCEKCHPGTFTKDNLYDACLILCSTCDKQDMVADCSATS 120  
 QY 121 DRKQCRTGLYY 133  
 DB 121 DRKQCRTGLYY 133

RESULT 8  
 ADJ45750  
 ID ADJ45750 standard; protein; 133 AA.

XX AC ADJ45750;  
 XX DT 06-MAY-2004 (first entry)  
 XX DE Murine tmst2 00004-d1 polypeptide.  
 XX KW Mouse; tmst2-receptor; tmst2 00004-d1;  
 KW acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease;  
 KW cachexia; cancer; cerebral malaria; diabetes mellitus;  
 KW disseminated intravascular coagulation; haemorrhagic shock; hepatitis;  
 KW insulin resistance; leprosy; leukaemia; lymphoma; meningitis;  
 KW multiple sclerosis; ischaemia; obesity; organ rejection;  
 KW rheumatoid arthritis; septic shock; stroke;  
 KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;  
 KW receptor.  
 XX OS Mus musculus.  
 XX PN US2004018544-A1.  
 XX PD 29-JAN-2004.  
 XX PF 17-JUL-2003; 2003US-00622407.  
 XX PR 09-JUL-1999; 99US-0143063P.  
 XX PR 07-JUL-2000; 2000US-00612033.  
 XX PA (SARI/) SARIS C.  
 XX PI Saris C;  
 XX DR WPI; 2004-224390/21.  
 XX DR N-PSDB; ADJ45749.  
 XX PT Novel tmst2-receptor polypeptide useful for diagnosing and treating  
 PT disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial  
 XX infections.

PS Example 1; SEQ ID NO 6; 57pp; English.  
 XX The invention relates to a tmst2-receptor polypeptides and the  
 CC polynucleotide encoding them. The sequences of the invention are useful  
 CC for treating diseases and conditions including acquired immunodeficiency  
 CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral  
 CC malaria, diabetes mellitus, disseminated intravascular coagulation,  
 CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,  
 CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ  
 CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory  
 CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.  
 CC This sequence represents a murine tmst2-receptor polypeptide clone of the  
 CC invention.  
 XX  
 SQ Sequence 133 AA;

Query Match 68.8%; Score 748; DB 8; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 5.9e-54;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 DB 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 QY 61 KNCAGTFVKAPCEIPHTQOCEKCHPGTFTKDNLYDACLILCSTCDKQDMVADCSATS 120  
 DB 61 KNCAGTFVKAPCEIPHTQOCEKCHPGTFTKDNLYDACLILCSTCDKQDMVADCSATS 120  
 QY 121 DRKQCRTGLYY 133  
 DB 121 DRKQCRTGLYY 133

RESULT 9  
 AAW80254  
 ID AAW80254 standard; protein; 176 AA.

XX AC AAW80254;  
 XX DT 28-JAN-1999 (first entry)  
 XX DE Amino acid sequence of protein 7F4.  
 XX KW Protein 7F4; differentiation; osteoblast cell; bone growth; bone sarcoma.  
 XX OS Unidentified.  
 XX PH Key Location/Qualifiers  
 FT Peptide 1..28 /note= "signal peptide"  
 FT Protein 29..176 /note= "mature protein"  
 XX WO9843998-A1.  
 XX PD 08-OCT-1998.  
 XX PF 01-APR-1998; 98WO-JP001511.  
 XX PR 01-APR-1997; 97JP-00099653.  
 XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.  
 XX PI Kimura N, Toyoshima T;  
 XX DR WPI; 1998-568275/48.  
 XX DR N-PSDB; AAV68046.  
 XX PT Receptor protein inducing differentiation in osteoblast cells - has  
 PT extracellular region only and can be used for screening substances for  
 PT treatment of bone growth disorders.  
 XX Claim 1; Page 29-31; 51pp; Japanese.

CC The present sequence represents a protein designated 7F4. This protein is  
 CC capable of inducing differentiation in osteoblast cells. The protein may  
 CC be used to screen compounds for the ability to bind to it, for use as  
 CC ligands, agonists or antagonists and inhibiting or otherwise altering its  
 CC differentiation inducing activity. Compounds so identified, as well as  
 CC the protein itself, DNA encoding it, and antibodies to it, may be used in  
 CC the treatment of diseases of bone growth and osteoblast differentiation,  
 CC such as bone sarcomas  
 CC  
 CC Sequence 176 AA:  
 SQ

CC The invention relates to transmembrane decoy receptor, ymkz5 belonging to  
CC tumour necrosis factor (TNF) receptor supergene family and nucleic acid  
CC sequences encoding such receptors. The invention is useful for detecting  
CC diseases or susceptibility to diseases related to the presence of mutated  
CC ymkz5-receptor gene such as tumours or cancers. The sequences of the  
CC invention are used as medication for a number of diseases such as  
CC acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases,  
CC cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial  
CC ischaemia, obesity etc. The invention is also useful in gene therapy. The  
CC present sequence is mouse ymkz5 receptor protein.  
xx  
SO Sequence 176 AA:



Db 1 AMPESYSFNCNPDGEYQSNVDCCKTCSPTGTFVKAPCKIPHTQOQCEKCHPGTFTGKDNGLH 60  
 QY 99 ACILCSTCDKQEMVADCSATSDRKCQCRGTGLYYDDPKPESCRPTCKPQGIPLVQECN 158  
 Db 61 DCELSTCDKQEMVADCSATSDRKCQCEQIGLYYYDPKPPESCRPTCKPQGIPLVQECN 120  
 QY 159 STANTVCSVSNPNRFLFLLSPLSVLVSVVVPRI 195  
 Db 121 STANTVCSVSNPNRFLFLM-----LIVFCI 148

RESULT 14  
 ABG09344  
 ID ABG09344 standard; protein; 380 AA.  
 AC ABG09344;  
 DT 13-FEB-2002 (first entry)  
 XX Novel human diagnostic protein #9335.  
 DE Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder.  
 XX Homo sapiens.  
 OS  
 XX WO200175067-A2.  
 PN 11-OCT-2001.  
 PD 30-MAR-2001; 2001WO-US008631.  
 XX 31-MAR-2000; 2000US-00540217.  
 PR 23-AUG-2000; 2000US-00649167.  
 XX (HYSE-) HYSEQ INC.  
 PA Drmanac RT, Liu C, Tang YT;  
 PI WPI; 2001-639362/73.  
 DR N-PSDB; AAS73531.  
 XX New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.  
 XX Claim 20; SEQ ID NO 39703; 103pp; English.  
 PS The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG030377 represent novel human diagnostic  
 CC amino acid sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 380 AA;  
 SQ

Query Match 49.9%; Score 542.5; DB 4; Length 380;  
 Best Local Similarity 80.2%; Pred. No. 1.5e-36;  
 Matches 101; Conservative 0; Mismatches 0; Indels 25; Gaps 1;  
 QY 8 LVSSLSRWFLWRRLLLLLLLLLLLLLPLQ-----VKFAMLE 42  
 Db 47 LVSSLSRWFLWRRLLLLLLLLLLLLLPLQKAVHRKATPESAIADCSGRDCAFWKVFAMLE 106  
 QY 43 LHSFKCPAGEYWSKDVCKKCSAGTFVKAPCEIPHTQOQCEKCHPGTFTGKDNLDACIL 102  
 Db 107 LHSFKCPAGEYWSKDVCKKCSAGTFVKAPCEIPHTQOQCEKCHPGTFTGKDNLDACIL 166  
 QY 103 CSTCDK 108  
 Db 167 CSTCDK 172

RESULT 15  
 ADF57549  
 ID ADF57549 standard; protein; 117 AA.  
 XX ADF57549;  
 AC ADF57549;  
 DT 12-FEB-2004 (first entry)  
 XX Mouse ymkz5 receptor from clone ymkz5-00013-g11.  
 DE Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour;  
 KW cancer; acquired immune deficiency syndrome; AIDS; anaemia;  
 KW autoimmune disease; cachexia; leprosy; leukaemia; hepatitis;  
 KW multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;  
 KW receptor.  
 XX Mus musculus.  
 OS US2003096355-A1.  
 PN 22-MAY-2003.  
 PD 11-JUL-2002; 2002US-00193616.  
 XX 09-JUL-1999; 99US-0143137P.  
 PR 07-JUL-2000; 2000US-00611989.  
 XX (ZHAN/) ZHANG K.  
 PA Zhang K;  
 PI WPI; 2004-008943/01.  
 DR N-PSDB; ADF57563.  
 XX Novel ymkz5-receptor polypeptide useful for treating diseases such as  
 PT tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy,  
 PT leukemia, hepatitis, multiple sclerosis.  
 XX Example 1; SEQ ID NO 6; 57pp; English.  
 PS The invention relates to transmembrane decoy receptor, ymkz5 belonging to  
 CC tumour necrosis factor (TNF) receptor supergene family and nucleic acid  
 CC sequences encoding such receptors. The invention is useful for detecting  
 CC diseases or susceptibility to diseases related to the presence of mutated  
 CC ymkz5-receptor gene such as tumours or cancers. The sequences of the  
 CC invention are used as medication for a number of diseases such as  
 CC acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases,  
 CC cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial  
 CC ischaemia, obesity etc. The invention is also useful in gene therapy. The  
 CC present sequence is mouse ymkz5 receptor protein.  
 XX Sequence 117 AA;  
 SQ

Query Match 43.0%; Score 467; DB 8; Length 117;  
 Best Local Similarity 73.6%; Pred. No. 7.6e-31;  
 Matches 89; Conservative 5; Mismatches 19; Indels 8; Gaps 1;

Qy	7	SLVSSLSRWFLRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCAG	66
Db	5	SHVSSLSHWF-----LLLLLLNLFLPVIFAMPESYSFNCPPDGEYQSNNDVCCKTCPSG	56
Qy	67	TFVKAPCEIPHTOGQCEKCHPGTFTEKDNYLDACILGCTCDKDOEMVADCSATSDRKCC	126
Db	57	TFVKAPCKIPHTOGQCEKCHPGFTTGKONGLHDCELCSTCDKQNMVADCSATSDRKCEC	116
Qy	127	R	127
Db	117	Q	117

Search completed: September 9, 2005, 08:53:49  
Job time : 599.714 secs



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Result No.	Score	Query		DB	ID	Description
		Match	\$			
1	1087	100.0		198	4	US-09-612-033B-8
2	962	88.5		398	4	US-09-612-033B-14
3	956	87.9		180	4	US-09-612-033B-10
4	748	68.8		133	4	US-09-612-033B-6
5	746.5	68.7		176	3	US-09-411-722-1
6	746.5	68.7		176	4	US-09-855-266A-1
7	682.5	62.8		148	3	US-09-411-722-2
8	682.5	62.8		148	4	US-09-855-266A-2
9	218.5	20.1		327	3	US-09-290-640-66
10	218.5	20.1		327	4	US-09-665-615B-66
11	212.5	19.5		123	4	US-09-855-266A-13
12	208.5	19.2		355	1	US-08-292-549-6
13	208.5	19.2		355	3	US-09-006-353A-14
14	208.5	19.2		355	4	US-09-573-986-14
15	207.5	19.1		285	3	US-08-804-166-6
16	207.5	19.1		285	4	US-08-910-991-6
17	207.5	19.1		285	3	US-09-756-186-6
18	203.5	18.7		256	3	US-08-804-166-2
19	203.5	18.7		256	4	US-08-910-991-2
20	203.5	18.7		256	3	US-09-756-186-2
21	203.5	18.7		307	3	US-08-804-166-4
22	203.5	18.7		307	4	US-08-910-991-4
23	203.5	18.7		307	4	US-09-756-186-4
24	203.5	18.7		336	3	US-08-804-166-8
25	203.5	18.7		336	3	US-08-910-991-8
26	203.5	18.7		336	4	US-09-756-186-8
27	202.5	18.6		199	1	US-08-050-319B-48

```
; TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily
; FILE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
US-09-612-033B-14

Query Match      88.5%; Score 962; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.6e-81;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDYNDACILCSTCDKQEMVADCSATS 120
Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDYNDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRTGLYYDPKFPESCRCPTCKPQGPVLQECNSTANTVCSSSVS 171
Db 121 DRKQCRTGLYYDPKFPESCRCPTCKPQGPVLQECNSTANTVCSSSVS 171

RESULT 3
US-09-612-033B-10
; Sequence 10, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily
; FILE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-612-033B-10

Query Match      87.9%; Score 956; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 6.8e-81;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDYNDACILCSTCDKQEMVADCSATS 120
Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDYNDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRTGLYYDPKFPESCRCPTCKPQGPVLQECNSTANTVCSSSVS 170
Db 121 DRKQCRTGLYYDPKFPESCRCPTCKPQGPVLQECNSTANTVCSSSVS 170

; TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily
; FILE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-612-033B-14

Query Match      88.5%; Score 962; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 4.6e-81;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDYNDACILCSTCDKQEMVADCSATS 120
Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDYNDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRTGLYYDPKFPESCRCPTCKPQGPVLQECNSTANTVCSSSVS 171
Db 121 DRKQCRTGLYYDPKFPESCRCPTCKPQGPVLQECNSTANTVCSSSVS 171
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RESULT 4
US-09-612-033B-6
; Sequence 6, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmst2, a No. 6627199el Member of the TNF-Receptor Superfamily
; FILE OF INVENTION: of Genes
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-612-033B-6

Query Match      68.8%; Score 748; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 8.1e-62;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDYNDACILCSTCDKQEMVADCSATS 120
Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDYNDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRTGLYY 133
Db 121 DRKQCRTGLYY 133

RESULT 5
US-09-411-722-1
; Sequence 1, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501/040001
; CURRENT APPLICATION NUMBER: US/09/411,722
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-1

Query Match      68.7%; Score 746.5; DB 3; Length 176;
Best Local Similarity 75.1%; Pred. No. 1.5e-61;
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;

Qy 7 SLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNC 66
Db 5 SHVSSLSHWF-----LLLLLLNLFPLVIFAMPESYSFNCPPDGEYQSNDCVCKTCS 56

Qy 67 TFVKAPCEIPHTQGCCKCHPGTFTKDYNDACILCSTCDKQEMVADCSATSDRKQC 126
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Db 57 TFKVAPCKIHTQGCCKCHPGFTGDKNGLHDCSTCDKQNMWVADCSATSDRKCEC 116  
Qy 127 RTGLYYDDPKFPSCRCCTKCPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186  
Db 117 QIGLYYYDDPKFPSCRCCTKCPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLM----- 170  
Qy 187 IVSVVVFRI 195  
Db 171 ---LIVFCI 176

## RESULT 6

US-09-855-266A-1  
; Sequence 1, Application US/09855266A  
; Patent No. 6784284  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501-040002  
; CURRENT APPLICATION NUMBER: US/09/855,266A  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 09/411,722  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-855-266A-1

Query Match 68.7%; Score 746.5; DB 4; Length 176;  
Best Local Similarity 75.1%; Pred. No. 1.5e-61;  
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;

Qy 7 SLVSSLRWFLRRLRLLLLLNLPLOVKFAMLEHSPKPAGEYWSKDVCKKCSAG 66  
Db 5 SHVSSLSHW- - - - - LLLLLNLPVIFAMPESYSFNCPSGPDGEYQSDNVCCKTSPG 56  
Qy 67 TFKVAPCKIHTQGCCKCHPGFTGDKNGLHDCSTCDKQNMWVADCSATSDRKCEC 126  
Db 57 TFKVAPCKIHTQGCCKCHPGFTGDKNGLHDCSTCDKQNMWVADCSATSDRKCEC 116  
Qy 127 RTGLYYDDPKFPSCRCCTKCPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186  
Db 117 QIGLYYYDDPKFPSCRCCTKCPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLM----- 170  
Qy 187 IVSVVVFRI 195  
Db 171 ---LIVFCI 176

## RESULT 7

US-09-411-722-2  
; Sequence 2, Application US/09411722  
; Patent No. 6271366  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501/040001  
; CURRENT APPLICATION NUMBER: US/09/411,722  
; CURRENT FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01

; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-411-722-2

Query Match 62.8%; Score 682.5; DB 3; Length 148;  
Best Local Similarity 78.3%; Pred. No. 1e-55;  
Matches 123; Conservative 8; Mismatches 17; Indels 9; Gaps 1;

Qy 39 AMLEHSPKPAGEYWSKDVCKKCSAGTFVKAPCIPIHTQGCCKCHPGFTGDKNGLH 98  
Db 1 AMPESYSFNCPSGPDGEYQSDNVCCKTSPGTFVKAPCIPIHTQGCCKCHPGFTGDKNGLH 60  
Qy 99 ACILCSTCDKQNMWVADCSATSDRKCCQIGLYYYDDPKFPSCRCCTKCPQGIPLVQECN 158  
Db 61 DCELCSTCDKQNMWVADCSATSDRKCCQIGLYYYDDPKFPSCRCCTKCPQGIPLVQECN 120  
Qy 159 STANTVCSSSVSNPRNRLFLLLSPLSVLVVVFRI 195  
Db 121 STANTVCSSSVSNPRNRLFLLM-----LIVFCI 148

## RESULT 8

US-09-855-266A-2  
; Sequence 2, Application US/09855266A  
; Patent No. 6784284  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501-040002  
; CURRENT APPLICATION NUMBER: US/09/855,266A  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 09/411,722  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 148  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-855-266A-2

Query Match 62.8%; Score 682.5; DB 4; Length 148;  
Best Local Similarity 78.3%; Pred. No. 1e-55;  
Matches 123; Conservative 8; Mismatches 17; Indels 9; Gaps 1;

Qy 39 AMLEHSPKPAGEYWSKDVCKKCSAGTFVKAPCIPIHTQGCCKCHPGFTGDKNGLH 98  
Db 1 AMPESYSFNCPSGPDGEYQSDNVCCKTSPGTFVKAPCIPIHTQGCCKCHPGFTGDKNGLH 60  
Qy 99 ACILCSTCDKQNMWVADCSATSDRKCCQIGLYYYDDPKFPSCRCCTKCPQGIPLVQECN 158  
Db 61 DCELCSTCDKQNMWVADCSATSDRKCCQIGLYYYDDPKFPSCRCCTKCPQGIPLVQECN 120  
Qy 159 STANTVCSSSVSNPRNRLFLLLSPLSVLVVVFRI 195  
Db 121 STANTVCSSSVSNPRNRLFLLM-----LIVFCI 148

## RESULT 9

US-09-290-640-66  
; Sequence 66, Application US/09290640  
; Patent No. 6204055  
; GENERAL INFORMATION:  
; APPLICANT: Dean, Nicholas M.

Query Match	20.1%; Score 218.5; DB 4; Length 327;
Best Local Similarity	30.0%; Pred. No. 1.9e-12;
Matches	57; Conservative 30; Mismatches 74; Indels 29; Gaps 8
QY	32 LPLQVKFAMLELH-----SFK-----CPAGEYSKDVCKKNCAGTFVKA 71
Db	8 LPFLVLGSLRLVHTGTNSESILRRRVHETDKCSEGLYOGGFCCQPQPGKKVE 67
QY	72 PCBIPTTGGCEKCHPG-TFTKEKNYLADCLGSTCDKQ--EMWADCATSDDRCQCT 128
Db	68 DCKMNGGTPCAPCTEGEYMDKNHYADKRRCTLCDDEHGLEIVETNCTLTQNTCKCKP 127
QY	129 GLYYVDPKPPESCRCCTKCGOIGPVLOECKNSTANTWCSSVSNPRLFIILSPISLVIT 188
Db	128 D-FYCDSPGCHEHCVCASCHEG--TLFPCTATSNINCRK--QSFRNLW-LUTILLVLLIP 181
QY	189 SVVVFRIIR 198

```

; FILING DATE: 10/19/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2602-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-292-549--6

Query Match          19.2%; Score 208.5; DB 1; Length 355;
Best Local Similarity 33.8%; Pred. No. 1.7e-11;
Matches 51; Conservative 21; Mismatches 68; Indels 11; Gaps 6;

YQ 21 LLLLLLLLLLPLQVKFAMLEHSPKAGYWSDVCCNCKNSAGTFVKAPCEI-PHTQ 79
DB 7 LLLLSIIILNSDITPH----EPSNGKCKDNEYKRHHLCCLSCPPGTVASRLCDSKTNTN 62
YQ 80 GOCEKHCHPGTFTTEKNYLDAICLCS-TCDKDQMADVADGSAISDRKCQCRTGLYYDPKFP 138
DB 63 TQCTPCASDTFTSRNNHLPAFLSCNCRCDNQVETRSCNTTHNRICDCAPG-YYCFLKGS 121
YQ 139 ESCRPC---TKCPQGIPVLQECNSTANTVCS 166
DB 122 SGCKACVSQTCKIGYGVS GH-TPTGDVVCS 151

RESULT 13
US-09-006-353A-14
; Sequence 14, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear

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;  
; COUNTRY: USA  
; ZIP: 22207  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/804,166  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/011,936  
; FILING DATE: 20 February 1996  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: CAMPBELL-2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 285 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-804-166-6

Query Match 19.1%; Score 207.5; DB 3; Length 285;  
Best Local Similarity 34.4%; Pred. No. 1.7e-11;  
Matches 53; Conservative 17; Mismatches 71; Indels 13; Gaps 6;  
  
QY 20 RLLLLLLLLLNLPLQVKFAMLELHSPKCPAGEY---WSKDVCCCKNCAGTFVKAPCEI 75  
Db 2 RLSLLAFGLLCLPLWQBSA-----DSVCPQGYIHPQNNISICCTKCHKGTLYLNDPCG 56  
  
QY 76 PHTQGCCKCHPGTTFTEKDNVLDACILCSTCDKD--QEMVADCSATSDRKCCQRTGLY-Y 132  
Db 57 PQQDTDCRECSGSPFASENHLRHLCLSCSKCKEMGQVEISSCTVDRTVCGCRKNQYRH 116  
  
QY 133 YDPKPEPESCRCTKCPGIPVLQECNSTANTVCS 166  
Db 117 YNSENLFQCFNCTCLNG-TVHLSCQEKONTVCT 149

Search completed: September 9, 2005, 09:35:53  
Job time : 127.81 secs



	Query Match	100.0%;	Score 1087;	DB 15;	Length 198;
	Best Local Similarity	100.0%;	Pred. No. 1.2e-87;		
	Matches 198;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	MGFFCSLVSSLSRWFLRRLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKPAGEYWSKDVC	60		
Db	1	MGFFCSLVSSLSRWFLRRLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKPAGEYWSKDVC	60		
Qy	61	KXCSAGTFVKAPCEIPHTQGCCKCHPGTTEKONYLDACILCSTCKDQEMVADCATS	120		
Db	61	KXCSAGTFVKAPCEIPHTQGCCKCHPGTTEKONYLDACILCSTCKDQEMVADCATS	120		

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QY 121 DRKQCRRTGLYYDYPKFPESCRCPTKCPQGIPLVQECNSTANTVCSVSNPRNRLFLLL 180
DB 121 DRKQCRRTGLYYDYPKFPESCRCPTKCPQGIPLVQECNSTANTVCSVSNPRNRLFLLL 180
QY 181 SPLSVLIIVSVVFRIR 198
DB 181 SPLSVLIIVSVVFRIR 198

RESULT 2
US-10-622-407-14
; Sequence 14, Application US/10622407
; Publication No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US/10/622,407
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US 09/612,033
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: Immunoglobulin sequences
US-10-622-407-14

Query Match 88.5%; Score 962; DB 15; Length 398;
Best Local Similarity 100.0%; Pred. No. 2.4e-76;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVCC 60
DB 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVCC 60
QY 61 KNCAGTFVKAPCEIPHTQGQCEKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPHTQGQCEKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKQCRRTGLYYDYPKFPESCRCPTKCPQGIPLVQECNSTANTVCSVSN 171
DB 121 DRKQCRRTGLYYDYPKFPESCRCPTKCPQGIPLVQECNSTANTVCSVSN 171

RESULT 3
US-10-622-407-10
; Sequence 10, Application US/10622407
; Publication No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US/10/622,407
; PRIOR FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US 09/612,033
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 180
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-622-407-10

Query Match 88.8%; Score 748; DB 15; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.2e-58;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVCC 60
DB 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVCC 60
QY 61 KNCAGTFVKAPCEIPHTQGQCEKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPHTQGQCEKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKQCRRTGLYY 133
DB 121 DRKQCRRTGLYY 133

RESULT 5
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
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; TYPE: PRT
; ORGANISM: Mus musculus
US-10-622-407-10

Query Match 87.9%; Score 956; DB 15; Length 180;
Best Local Similarity 100.0%; Pred. No. 3.6e-76;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVCC 60
DB 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVCC 60
QY 61 KNCAGTFVKAPCEIPHTQGQCEKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPHTQGQCEKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKQCRRTGLYYDYPKFPESCRCPTKCPQGIPLVQECNSTANTVCSVSN 170
DB 121 DRKQCRRTGLYYDYPKFPESCRCPTKCPQGIPLVQECNSTANTVCSVSN 170

RESULT 4
US-10-622-407-6
; Sequence 6, Application US/10622407
; Publication No. US20040018544A1
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NO
; FILE REFERENCE: 01017/35434B
; CURRENT APPLICATION NUMBER: US/10/622,407
; CURRENT FILING DATE: 2003-07-17
; PRIOR APPLICATION NUMBER: US 09/612,033
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-622-407-6

Query Match 68.8%; Score 748; DB 15; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.2e-58;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVCC 60
DB 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLELHLSFKCPAGEYWSKDVCC 60
QY 61 KNCAGTFVKAPCEIPHTQGQCEKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPHTQGQCEKCHPGTFTKDNLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKQCRRTGLYY 133
DB 121 DRKQCRRTGLYY 133

RESULT 5
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
```

; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-09-855-266A-1

Query Match 68.7%; Score 746.5; DB 9; Length 176;  
Best Local Similarity 75.1%; Pred. No. 9.3e-58;  
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;  
QY 7 SLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCKNCAG 66  
Db 5 SHVSSLSHWF-----LLLLLLNLFPLVIFAMPESYSFNCPPGEGYQSDVCKCTCPG 56  
QY 67 TFVKAPCEIPTHQOQCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126  
Db 57 TFVKAPCKIPTHQOQCEKCHPGTFTGKONGLHDCELCSTCDKQNMVADCSATSDRKCEC 116  
QY 127 RTGLYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186  
Db 117 QIGLYYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLM----- 170  
QY 187 IVSVVVFRI 195  
Db 171 ---LIVFCI 176

RESULT 6  
US-10-193-616-8  
; Sequence 8, Application US/10193616  
; Publication No. US20030096355A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Ke  
; TITLE OF INVENTION: Isolation, Identification, and Characterization of  
; TITLE OF INVENTION: ymkz5, a novel  
; FILE REFERENCE: member of the TNF-Receptor Supergene Family  
; CURRENT APPLICATION NUMBER: US/10/193,616  
; PRIOR FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: US/09/611,989  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/143,137  
; PRIOR FILING DATE: 1999-07-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 8  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-193-616-8

Query Match 68.7%; Score 746.5; DB 14; Length 176;  
Best Local Similarity 75.1%; Pred. No. 9.3e-58;  
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;  
QY 7 SLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCKNCAG 66  
Db 5 SHVSSLSHWF-----LLLLLLNLFPLVIFAMPESYSFNCPPGEGYQSDVCKCTCPG 56  
QY 67 TFVKAPCEIPTHQOQCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126  
Db 57 TFVKAPCKIPTHQOQCEKCHPGTFTGKONGLHDCELCSTCDKQNMVADCSATSDRKCEC 116  
QY 127 RTGLYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186  
Db 117 QIGLYYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLM----- 170

QY 187 IVSVVVFRI 195  
Db 171 ---LIVFCI 176

## RESULT 7

US-10-802-332-1  
; Sequence 1, Application US/10802332  
; Publication No. US20040152879A1  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501-040002  
; CURRENT APPLICATION NUMBER: US/10/802,332  
; CURRENT FILING DATE: 2004-03-16  
; PRIOR APPLICATION NUMBER: US/09/855,266  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 09/411,722  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 176  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-802-332-1

Query Match 68.7%; Score 746.5; DB 16; Length 176;  
Best Local Similarity 75.1%; Pred. No. 9.3e-58;  
Matches 142; Conservative 8; Mismatches 22; Indels 17; Gaps 2;  
QY 7 SLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCKNCAG 66  
Db 5 SHVSSLSHWF-----LLLLLLNLFPLVIFAMPESYSFNCPPGEGYQSDVCKCTCPG 56  
QY 67 TFVKAPCEIPTHQOQCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126  
Db 57 TFVKAPCKIPTHQOQCEKCHPGTFTGKONGLHDCELCSTCDKQNMVADCSATSDRKCEC 116  
QY 127 RTGLYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLLSPLSVL 186  
Db 117 QIGLYYYDDPKFPESCRCPTCKPQGIPLVQECNSTANTVCSSSVSNPRNRLFLLM----- 170  
QY 187 IVSVVVFRI 195  
Db 171 ---LIVFCI 176

## RESULT 8

US-10-193-616-14  
; Sequence 14, Application US/10193616  
; Publication No. US20030096355A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Ke  
; TITLE OF INVENTION: Isolation, Identification, and Characterization of  
; TITLE OF INVENTION: ymkz5, a novel  
; FILE REFERENCE: member of the TNF-Receptor Supergene Family  
; CURRENT APPLICATION NUMBER: US/10/193,616  
; CURRENT FILING DATE: 2002-07-11  
; PRIOR APPLICATION NUMBER: US/09/611,989  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/143,137  
; PRIOR FILING DATE: 1999-07-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 14

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; LENGTH: 396
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: ymkz5-Fc fusion protein
US-10-193-616-14

Query Match      65.4%; Score 711; DB 14; Length 396;
Best Local Similarity 80.0%; Pred. No. 2.8e-54;
Matches 132; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

Qy 7 SLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCCCKNSAG 66
Db 5 SHVSSLSHWF-----LLLLLLLPLVIFAMPESYSFNCPCGGEYQSDNVCKTCPSG 56

Qy 67 TFVKAPCEIPHTQOCEKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATSDRKQC 126
Db 57 TFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

Qy 127 RTGLYYDPKPPESCRPCTKCPQIGIPVLQECNSTANTVCSSSVSN 171
Db 117 QIGLYYDPKPPESCRPCTKCPQIGIPVLQECNSTANTVCSSSVSN 161

RESULT 9
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-2

Query Match      62.8%; Score 682.5; DB 9; Length 148;
Best Local Similarity 78.3%; Pred. No. 3.3e-52;
Matches 123; Conservative 8; Mismatches 17; Indels 9; Gaps 1;

Qy 39 AMLEHSPKCPAGEYWSKDVCCCKNSAGTFVKAPCEIPHTQOCEKCHPGTFTKDNLYD 98
Db 1 AMPESYSFNCPCDGEYQSDNVCKTCPSGTFVKAPCKIPHTQOCEKCHPGTFTGKDNGLH 60

Qy 99 ACILCSTCDKQEMVADCSATSDRKQCQRTGLYYDPKPPESCRPCTKCPQIGIPVLQECN 158
Db 61 DCELCSTCDKQNMVADCSATSDRKCECQIGLYYDPKPPESCRPCTKCPQIGIPVLQECN 120

Qy 159 STANTVCSSSVSNPRNRLFLLLSPLSVLIVSVVVFRI 195
Db 121 STANTVCSSSVSNPRNWLFLM-----LIVFCI 148

RESULT 11
US-10-193-616-6
; Sequence 6, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 117
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-193-616-6

Query Match      43.0%; Score 467; DB 14; Length 117;
Best Local Similarity 73.6%; Pred. No. 2.3e-33;
Matches 89; Conservative 5; Mismatches 19; Indels 8; Gaps 1;

Qy 7 SLVSSLSRWFLWRRLLLLLLLLLPLQVKFAMLEHSPKCPAGEYWSKDVCCCKNSAG 66
Db 5 SHVSSLSHWF-----LLLLLLLPLVIFAMPESYSFNCPCDGEYQSDNVCKTCPSG 56

Qy 67 TFVKAPCEIPHTQOCEKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATSDRKQC 126
Db 57 TFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116
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QY 127 R 127
Db 117 Q 117

RESULT 12
US-10-193-616-10
; Sequence 10, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: TNFRI
US-10-193-616-10

Query Match 20.8%; Score 226; DB 14; Length 247;
Best Local Similarity 27.4%; Pred. No. 7.7e-12;
Matches 59; Conservative 27; Mismatches 81; Indels 46; Gaps 6;

QY 21 LLLLLLLLLL-----PLQVKFAMLELHSPKCPAGEY---WSKDVCCNCSAGTFVKA 71
Db 11 LSLVLLALLMGHPSGVTGLVPSLGRKRDLSLCPQGYVHSKKNISICCTKCHKGTLYVS 70
QY 72 PCBIPHTQGCCKCHPGTFTTEKDNLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
Db 71 DCPSGRDTCRECEKGTFTTASQNYLRQCLSKCTCRKMSQVSPQADKDTVCCKEN 130
QY 130 LYY-YDPKPFESCRPTCKPQGIPLVQECNSTANTVCS----- 166
Db 131 QFORYLSETHFQVDCSPFCNG-TVTIPCKETQNTVCNCHAGFFLRESECVPCSHCKKNE 189
QY 167 -----SSVSNPRNRLFLLLSPLSLVI 187
Db 190 ECMKLCPLPPPLANVTNPQDSGTAVLLPLVILL 221

RESULT 13
US-10-410-012-3
; Sequence 3, Application US/10410012
; Publication No. US20030228276A1
; GENERAL INFORMATION:
; APPLICANT: Pitossi, Fernando J
; APPLICANT: Eisel, Ulrich L M
; TITLE OF INVENTION: Neuroprotective and neurodegenerative effects of long-term expres
; TITLE OF INVENTION: in the substantia nigra and a new model for Parkinson's disease
; FILE REFERENCE: 1418P US/101141-17
; CURRENT APPLICATION NUMBER: US/10/410,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/370,974
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-012-3

Query Match 20.8%; Score 226; DB 16; Length 454;
Best Local Similarity 27.4%; Pred. No. 1.4e-11;
Matches 58; Conservative 27; Mismatches 81; Indels 46; Gaps 6;

QY 21 LLLLLLLLLL-----PLQVKFAMLELHSPKCPAGEY---WSKDVCCNCSAGTFVKA 71
Db 11 LSLVLLALLMGHPSGVTGLVPSLGRKRDLSLCPQGYVHSKKNISICCTKCHKGTLYVS 70
QY 72 PCBIPHTQGCCKCHPGTFTTEKDNLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
Db 71 DCPSGRDTCRECEKGTFTTASQNYLRQCLSKCTCRKMSQVSPQADKDTVCCKEN 130
QY 130 LYY-YDPKPFESCRPTCKPQGIPLVQECNSTANTVCS----- 166
Db 131 QFORYLSETHFQVDCSPFCNG-TVTIPCKETQNTVCNCHAGFFLRESECVPCSHCKKNE 189
QY 167 -----SSVSNPRNRLFLLLSPLSLVI 187
Db 190 ECMKLCPLPPPLANVTNPQDSGTAVLLPLVILL 221

RESULT 14
US-10-799-345-24
; Sequence 24, Application US/10799345
; Publication No. US20040209316A1
; GENERAL INFORMATION:
; APPLICANT: Christopher T. Ritchlin
; APPLICANT: Sally Haas-Smith
; APPLICANT: Edward Schwarz
; TITLE OF INVENTION: Methods and Compositions Related to
; TITLE OF INVENTION: Joint Inflammation Diseases
; FILE REFERENCE: 21108.0031U2
; CURRENT APPLICATION NUMBER: US/10/799,345
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/454,573
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-799-345-24

Query Match 20.8%; Score 226; DB 16; Length 454;
Best Local Similarity 27.4%; Pred. No. 1.4e-11;
Matches 58; Conservative 27; Mismatches 81; Indels 46; Gaps 6;

QY 21 LLLLLLLLLL-----PLQVKFAMLELHSPKCPAGEY---WSKDVCCNCSAGTFVKA 71
Db 11 LSLVLLALLMGHPSGVTGLVPSLGRKRDLSLCPQGYVHSKKNISICCTKCHKGTLYVS 70
QY 72 PCBIPHTQGCCKCHPGTFTTEKDNLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
Db 71 DCPSGRDTCRECEKGTFTTASQNYLRQCLSKCTCRKMSQVSPQADKDTVCCKEN 130
QY 130 LYY-YDPKPFESCRPTCKPQGIPLVQECNSTANTVCS----- 166
Db 131 QFORYLSETHFQVDCSPFCNG-TVTIPCKETQNTVCNCHAGFFLRESECVPCSHCKKNE 189
QY 167 -----SSVSNPRNRLFLLLSPLSLVI 187
Db 190 ECMKLCPLPPPLANVTNPQDSGTAVLLPLVILL 221

RESULT 15
US-09-948-018-18
; Sequence 18, Application US/09948018
; Patent No. US20020150977A1
```

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Query Match 20.8%; Score 226; DB 15; Length 454;
Best Local Similarity 27.4%; Pred. No. 1.4e-11;
Matches 58; Conservative 27; Mismatches 81; Indels 46; Gaps 6;

QY 21 LLLLLLLLLL-----PLQVKFAMLELHSPKCPAGEY---WSKDVCCNCSAGTFVKA 71
Db 11 LSLVLLALLMGHPSGVTGLVPSLGRKRDLSLCPQGYVHSKKNISICCTKCHKGTLYVS 70
QY 72 PCBIPHTQGCCKCHPGTFTTEKDNLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
Db 71 DCPSGRDTCRECEKGTFTTASQNYLRQCLSKCTCRKMSQVSPQADKDTVCCKEN 130
QY 130 LYY-YDPKPFESCRPTCKPQGIPLVQECNSTANTVCS----- 166
Db 131 QFORYLSETHFQVDCSPFCNG-TVTIPCKETQNTVCNCHAGFFLRESECVPCSHCKKNE 189
QY 167 -----SSVSNPRNRLFLLLSPLSLVI 187
Db 190 ECMKLCPLPPPLANVTNPQDSGTAVLLPLVILL 221

RESULT 14
US-10-799-345-24
; Sequence 24, Application US/10799345
; Publication No. US20040209316A1
; GENERAL INFORMATION:
; APPLICANT: Christopher T. Ritchlin
; APPLICANT: Sally Haas-Smith
; APPLICANT: Edward Schwarz
; TITLE OF INVENTION: Methods and Compositions Related to
; TITLE OF INVENTION: Joint Inflammation Diseases
; FILE REFERENCE: 21108.0031U2
; CURRENT APPLICATION NUMBER: US/10/799,345
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/454,573
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-799-345-24

Query Match 20.8%; Score 226; DB 16; Length 454;
Best Local Similarity 27.4%; Pred. No. 1.4e-11;
Matches 58; Conservative 27; Mismatches 81; Indels 46; Gaps 6;

QY 21 LLLLLLLLLL-----PLQVKFAMLELHSPKCPAGEY---WSKDVCCNCSAGTFVKA 71
Db 11 LSLVLLALLMGHPSGVTGLVPSLGRKRDLSLCPQGYVHSKKNISICCTKCHKGTLYVS 70
QY 72 PCBIPHTQGCCKCHPGTFTTEKDNLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
Db 71 DCPSGRDTCRECEKGTFTTASQNYLRQCLSKCTCRKMSQVSPQADKDTVCCKEN 130
QY 130 LYY-YDPKPFESCRPTCKPQGIPLVQECNSTANTVCS----- 166
Db 131 QFORYLSETHFQVDCSPFCNG-TVTIPCKETQNTVCNCHAGFFLRESECVPCSHCKKNE 189
QY 167 -----SSVSNPRNRLFLLLSPLSLVI 187
Db 190 ECMKLCPLPPPLANVTNPQDSGTAVLLPLVILL 221

RESULT 15
US-09-948-018-18
; Sequence 18, Application US/09948018
; Patent No. US20020150977A1
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```
; GENERAL INFORMATION:
; APPLICANT: Theill et al
; TITLE OF INVENTION: TNF RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37677
; CURRENT APPLICATION NUMBER: US/09/948,018
; CURRENT FILING DATE: 2001-09-05
; PRIOR APPLICATION NUMBER: US 60/230,191
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-948-018-18

Query Match      20.1%; Score 218.5; DB 9; Length 204;
Best Local Similarity 30.0%; Pred. No. 2.9e-11;
Matches 57; Conservative 30; Mismatches 74; Indels 29; Gaps 8;

Qy 32 LPQVVFAMLELH-----SPK-----CPAGEYWSKDVCKKNCASAGTFVKA 71
Db 8 LPLVLGSQLRVHTQGTNSISESLKRRRVHETDKNCSEGLYQGPFCCQCPQFGKKVE 67

Qy 72 PCEIPHTQGOCEKCHPG--TFTEKKNYLDACILCTCDKQD--EMVADCSATSDRKCOCRT 128
Db 68 DCKMNGGTPTCAPCTEGKEYMDKNHYADKCRCTLCDEEHGLEVEVTNCTLTQNTKCKCP 127

Qy 129 GLYYDPKFPESCRPCTKCPQIPVLOECNSTANTVCSVSVSNPRNRLFLLLSLVLIV 188
Db 128 D-FYCDSPGCEHCVRASCSEHG--TLEPCTATSNINCRK--QSPNRRLW-LTLTLLVLLIP 181

Qy 189 SVVVFRIIR 198
Db 182 LVFIYRKYRK 191
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Search completed: September 9, 2005, 09:55:17  
Job time : 603.905 secs

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OM protein - protein search, using sw model

Run on: September 9, 2005, 06:50:20 ; Search time 143.524 Seconds  
(without alignments)  
132.737 Million cell updates/sec

Title: US-10-622-407-8

Perfect score: 1087

Sequence: 1 MFGFFCSLVSSLSRWFLWRR.....LLSPLSVLIVSVVVFRIIR 198

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	226	20.8	454	1 GQMS1	tumor necrosis fac
2	218.5	20.1	327	2 A46484	apoptosis-mediati
3	212.5	19.5	461	1 GQRT1	tumor necrosis fac
4	210	19.3	324	2 JC2395	Fas antigen precu
5	201.5	18.5	348	2 T28623	hypothetical prote
6	201.5	18.5	349	2 D36858	gene G4R protein -
7	201.5	18.5	349	2 D72175	G2R protein - vari
8	201.5	18.5	455	1 GQHUT1	tumor necrosis fac
9	200.5	18.4	461	2 JC4302	tumor necrosis fac
10	188	17.3	427	1 GQHUN	nerve growth facto
11	186.5	17.2	271	2 S12783	OX40 antigen precu
12	183.5	16.9	335	2 A40036	apoptosis-mediati
13	180.5	16.6	651	2 JC7705	death receptor-6 -
14	176.5	16.2	416	1 JN0006	nerve growth facto
15	175	16.1	314	2 I37393	FAS soluble protei
16	175	16.1	425	1 A26431	nerve growth facto
17	173.5	16.0	325	2 B43692	T2 protein - rabbi
18	173.5	16.0	461	1 A35356	tumor necrosis fac
19	167.5	15.4	326	1 GQVZML	T2 protein - myxom
20	162	14.9	272	2 I48700	gene ox40 protein
21	158.5	14.6	435	2 I54182	tumor necrosis fac
22	157.5	14.5	260	1 A46517	CD27 antigen precu
23	156	14.4	474	2 B38634	tumor necrosis fac
24	151.5	13.9	250	1 A49053	CD27 antigen precu
25	151.5	13.9	459	2 I48854	gene murine tumour
26	151	13.9	595	2 A42086	CD30 antigen precu
27	143	13.2	277	2 I37552	OX40 homolog - hum
28	126	11.6	1790	1 MMFF91	laminin beta-1 cha
29	123	11.3	256	2 B32393	T-cell antigen 4-1

30 122 11.2 305 2 A46476 B cell-associated  
31 121.5 11.2 493 2 JC5486 membrane glycoprot  
32 120.5 11.1 255 2 I38426 lymphocyte activat  
33 119.5 11.0 3635 2 T10053 laminin alpha 5 ch  
34 116 10.7 1193 2 A44018 laminin B2 chain  
35 116 10.7 4391 2 A38096 perlecan precursor  
36 114.5 10.5 1801 1 MMRTS laminin beta-2 cha  
37 114 10.5 1339 2 JC4387 epidermal growth f  
38 112 10.3 3707 2 S18252 heparan sulfate pr  
39 111.5 10.3 1609 1 MMHUB2 laminin gamma-1 ch  
40 111.5 10.3 4545 1 S25111 alpha-2-macroglobu  
41 111 10.2 1372 2 T25933 hypothetical prote  
42 111 10.2 1548 2 S34583 serine proteinase  
43 111 10.2 1786 1 MMWSB1 laminin beta-1 cha  
44 110.5 10.2 713 2 A35502 major surface-labe  
45 110 10.1 1192 2 S69000 laminin gamma 2 ch

#### ALIGNMENTS

#### RESULT 1

GQMS1

tumor necrosis factor receptor 1 precursor - mouse

N;Alternate names: tumor necrosis factor receptor, 55K

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence,revision 30-Jun-1992 #text change 09-Jul-2004

C;Accession: A38634; B40254; S16677; S19021; I54532; I57826

R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.; Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r

A;Reference number: A38634; MUID:91187885; PMID:1849278

A;Accession: A38634

A;Molecule type: mRNA

A;Residues: 1-454 <LEU>

A;Cross-references: NID:G199825; PIDN:AAA39751.1; PID:G199826

R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk

Mol. Cell. Biol. 11, 3020-3026, 1991

A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A;Reference number: A40254; MUID:91246168; PMID:1645445

A;Accession: B40254

A;Molecule type: mRNA

A;Residues: 1-454 <GO2>

A;Cross-references: GB:M60468; NID:G199825; PIDN:AAA39751.1; PID:G199826

R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissenerghis, A.M.; Gray, P.W.; Feldma

Eur. J. Immunol. 21, 1649-1656, 1991

A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis

A;Reference number: S16677; MUID:91285014; PMID:1647956

A;Accession: S16677

A;Molecule type: mRNA

A;Residues: 1-454 <BAR>

A;Cross-references: EMBL:X59238; NID:G53578; PIDN:CAA41922.1; PID:G53579

R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.

Immunogenetics 34, 338-340, 1991

A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.

A;Reference number: S19021; MUID:92039815; PMID:1657766

A;Accession: S19021

A;Molecule type: mRNA

A;Residues: 1-454 <ROT>

A;Cross-references: EMBL:X57796; NID:G54848; PIDN:CAA40936.1; PID:G54849

R;Bebo, B.F.

Immunogenetics 39, 450-451, 1994

A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1

A;Reference number: I54532; MUID:94245292; PMID:8188324

A;Accession: I54532

A;Status: translated from GB/EMBL/DBU

A;Molecule type: mRNA

A;Residues: 1-454 <RES>

A;Cross-references: GB:L26349; NID:G430732; PIDN:AAA59361.1; PID:G430733

R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.

Mol. Immunol. 30, 165-176, 1993

A;Title: Genomic organization and promoter function of the murine tumor necrosis factor

A;Reference number: I57826; MUID:93156721; PMID:8381516



F;44-79/Domain: NGF receptor repeat homology <NGF>  
F;81-124/Domain: NGF receptor repeat homology <NG4>

Query Match 20.1%; Score 218.5; DB 2; Length 327;  
Best Local Similarity 30.0%; Pred. No. 2.1e-09;  
Matches 57; Conservative 30; Mismatches 74; Indels 29; Gaps 8;

QY 32 LPQLQVFAMLELH-----SFK-----CPAGEYMSKDVCKKNCAGTFVKA 71  
DB 8 LPVLVAGSLRVHTVGTNSISLKLRRRVHETDKNCSEGLYOGGFPCCQPCPGKKKVE 67  
QY 72 PCBIPTQGCCKHPG-TFTEKNDYLDACILCSTCDKQ--EMVADCSATSDRKCCQRT 128  
DB 68 DCKWNGTPTCAPCTEGKEYMDKNHYADKRRCTLCDDEHGLEVETNCTLTQNTCKCKP 127  
QY 129 GLYYDPKPEPCRPCTKCPQGIPLVLEQNSTANTVCSSSVSNPRNRLFLLLSPLSLVIL 198  
DB 128 D-FYCDSPGCEHCVRASCSEHG--TLEPCTATNTNCRK--QSPRNRLW-LLTILVLLIP 181  
QY 189 SVVVFRIIR 198  
DB 182 LVFIKRYRK 191

RESULT 3  
GORTT1  
tumor necrosis factor receptor 1 precursor - rat  
N/Contains: tumor necrosis factor binding protein 1 (TNF blocking factor)  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 30-Jun-1992 #sequence\_revision 07-Oct-1994 #text\_change 09-Jul-2004  
C/Accession: B36555  
R:Himmeler, A.; Maurer-Pogoy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; DNA Cell Biol. 9, 705-715, 1990  
A/Title: Molecular cloning and expression of human and rat tumor necrosis factor receptor  
A/Reference number: A36555; MUID:91090841; PMID:1702293  
A/Accession: B36555  
A/Molecule type: mRNA  
A/Residues: 1-461 <HIM>  
A/Cross-references: UNIPROT:P22934; GB:M63122; NID:G207361; PIDN:AAA42256.1; PID:9207  
C/Comment: This protein is one of two known receptors for both TNF-alpha (cachectin)  
C/Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homology  
C/Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-461/Product: tumor necrosis factor receptor type 1 #status predicted <MAT>  
F;30-211/Domain: extracellular #status predicted <EXT>  
F;30-201/Product: tumor necrosis factor binding protein #status predicted <TPB>  
F;44-82/Domain: NGF receptor repeat homology <NG1>  
F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-204/Domain: NGF receptor repeat homology <NG4>  
F;212-234/Domain: transmembrane #status predicted <MSM>  
F;235-461/Domain: intracellular #status predicted <INT>  
F;54,151,201/Binding site: carbohydate (Asn) (covalent) #status predicted

Query Match 19.5%; Score 212.5; DB 1; Length 461;  
Best Local Similarity 26.0%; Pred. No. 7.6e-09;  
Matches 57; Conservative 31; Mismatches 86; Indels 45; Gaps 6;

QY 21 LLLLLLLLLLNL-----PLQVKFAMLELHLSFKPAGEY---WSKDVCKKNCAGTFVKA 71  
DB 11 LSLVALLAMGHIHPSGVTGLVPSLGDREKRDNLCPQGYAKHPKNNISICCTCKHGYLVS 70  
QY 72 PCBIPTQGCCKHPG-TFTEKNDYLDACILCSTCDK--QEMVADCSATSDRKCCQRTG 129  
DB 71 DCPSPGQETVCEYCDKGTFTASQHNVRQCLSCCKTCKEMPQVEISPKCADMDTVCGCKKN 130  
QY 130 LVY-YDPKPEPCRPCTKCPQGIPLVLEQNSTANTVCS-----166  
DB 131 QFORYLSETHFQVDCSPFENG-TVTIPCKEQNTVCNCHAGFFLSGNECTPCSHCKKNQ 189  
QY 167 -----SSVSNPRNRLFLLLSPLSLVSVVVFRI 195  
DB 190 ECMKCLPPVANTNPQDSGTAVLLPLVTLFLGLCLLFFI 228

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RESULT 4
Fc2395
C;Species: Rattus norvegicus (Norway rat)
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C;Accession: JC2395; PC2246
R;Kimura, K.; Wakatsuki, T.; Yamamoto, M.
Biochem. Biophys. Res. Commun. 198, 666-674, 1994
A;Title: A variant mRNA species encoding a truncated form of Fas antigen in the rat liver
A;Reference number: JC2395; MUID:94128114; PMID:7507668
A;Accession: JC2395
A;Molecule type: mRNA
A;Residues: 1-324 <KIM>
A;Cross-references: UNIPROT:Q63199; DDBJ:D26112; NID:g468486; PIDN:BAA05108.1; PID:d1005
A;Experimental source: thymus
A;Accession: PC2246
A;Molecule type: mRNA
A;Residues: 1-62, 'RFT' <K12>
A;Cross-references: DDBJ:D26113; NID:g468488; PIDN:BAA05109.1; PID:d1005651; PID:g468489
A;Experimental source: liver
C;Genetics:
A;Introns: 62/1
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog
C;Keywords: transmembrane protein
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-324/Product: Fas antigen #status predicted <MAT>
F;44-79/Domain: NGF receptor repeat homology <NGF>
F;81-124/Domain: NGF receptor repeat homology <NG4>
F;171-188/Domain: transmembrane #status predicted <TM>

Query Match 19.3%; Score 210; DB 2; Length 324;
Best Local Similarity 29.4%; Pred. No. 9.1e-09;
Matches 57; Conservative 30; Mismatches 79; Indels 28; Gaps 9;

QY 17 LWRRLRLRLRLRLPLQV-----FAMLELH-----SFKCPAGEYWSKDVCKNC 63
DB 2 LW--IMAVLPLVAGPELVNRMQGTDSIFEGLELKRVSRETNNCSGLYQVGFCCQPC 59
QY 64 SAGTFVKAPCEIPTHQGCCKHPGT----FTEKDYLDACILCSTCDKQ--EMVADCS 117
DB 60 QPGERKVKDCT--TSGAPTCPTGEBEYTRKHYSKRCRCAPCDGEGHLEVTNCT 116
QY 118 ATSDRKQCCTGLYYDPKFPESCRCPTCKPQGI-PVLQBCNSTANTVCSSSVSNPNRL 176
DB 117 RTQNTKRCRKEN-PYCNASLCDHCYHCTSC--GLEDLLEPCTRTSNTKCKKQSSNYKLLW 173
QY 177 FLLSLPSLVIVSV 190
DB 174 LLILPLGLAILFVFI 187

RESULT 5
T28623
hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004
C;Accession: T28623
R;Masung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin
Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus
A;Reference number: 220488; MUID:94088747; PMID:8264798
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-348 <MAS>
A;Cross-references: UNIPROT:P34015; EMBL:I22579; NID:g623595; PIDN:AAA60933.1; PID:g4391
A;Experimental source: strain Bangladesh 1975
C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology

Query Match 18.5%; Score 201.5; DB 2; Length 348;
Best Local Similarity 35.5%; Pred. No. 4.1e-08;

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Matches 44; Conservative 18; Mismatches 55; Indels 7; Gaps 5;
QY 47 KCPAGEYWSKDVCKNCAGTFVKAPCEIPTHQGCCKHPGTFTKDYLDACILCS-T 105
DB 30 KCKDTEYKRHNLCCLSCPPGTVASRLCD-SKNTQCTPCGSGTFTSRNNHLPACLSNGR 88
QY 106 CDKQDQEWVADCSATSDRKQCCTGLYYDPKFPESCRCPC---TKCPQGI-PVLQECNSTAN 162
DB 89 CNSNQVETRSCTNTHNRICECSPG-YVCLLKSGSGCKACVSTQTKCGIGYGVSGH-TSVGD 146
QY 163 TVCS 166
DB 147 VICS 150

RESULT 6
D36858
Gene G4R protein - variola virus
N;Alternate names: B28R protein (COP)
C;Species: variola virus
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: D36858; S46888; S32385; S35987
R;Blinov, V.M.
Submitted to GenBank, November 1992
A;Reference number: A36859
A;Accession: D36858
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <BLI>
A;Cross-references: UNIPROT:P34015; GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457087
A;Experimental source: strain India-1967, ssp. major, isolate Ind3
R;Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnjakov, S.G.; Chizhikov, V.E.; Frolov,
submitted to the EMBL Data Library, April 1992
A;Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
A;Reference number: S46868
A;Accession: S46888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-349 <KOL>
A;Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449
A;Experimental source: strain India-1967, isolate Ind3
R;Shchelkunov, S.N.; Blinov, V.M.; Sandakhchiev, L.S.
FEBS Lett. 319, 80-83, 1993
A;Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A;Reference number: S32385; MUID:93202281; PMID:8384129
A;Accession: S32385
A;Molecule type: DNA
A;Residues: 31-168 <SHC>
A;Cross-references: EMBL:X69198
A;Experimental source: strain India-1967, ssp. major
C;Genetics:
A;Gene: G4R
C;Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homology
F;32-66/Domain: NGF receptor repeat homology <NGF>
F;68-109/Domain: NGF receptor repeat homology <NG2>
F;110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 18.5%; Score 201.5; DB 2; Length 349;
Best Local Similarity 35.5%; Pred. No. 4.1e-08;
Matches 44; Conservative 18; Mismatches 55; Indels 7; Gaps 5;
QY 47 KCPAGEYWSKDVCKNCAGTFVKAPCEIPTHQGCCKHPGTFTKDYLDACILCS-T 105
DB 31 KCKDTEYKRHNLCCLSCPPGTVASRLCD-SKNTQCTPCGSGTFTSRNNHLPACLSNGR 89
QY 106 CDKQDQEWVADCSATSDRKQCCTGLYYDPKFPESCRCPC---TKCPQGI-PVLQECNSTAN 162
DB 90 CNSNQVETRSCTNTHNRICECSPG-YVCLLKSGSGCKACVSTQTKCGIGYGVSGH-TSVGD 147
QY 163 TVCS 166
DB 148 VICS 151

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A;Accession: JC2404  
A;Molecule type: protein  
A;Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>  
A;Experimental source: urine  
C;Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and  
C;Genetics:  
A;Gene: GDB:TNFR1  
A;Cross-references: GDB:125913; OMIM:191190  
A;Map position: 12p13.2-12p13.2  
A;Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog  
C;Keywords: duplication; glycoprotein; receptor; transmembrane protein  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;22-455/Product: tumor necrosis factor receptor 1 #status predicted <MAT>  
F;30-211/Domain: extracellular #status predicted <EXT>  
F;41-201/Product: TNF binding protein 1 (tumor necrosis factor alpha inhibitor) #status  
F;44-82/Domain: NGF receptor repeat homology <NG1>  
F;84-126/Domain: NGF receptor repeat homology <NG2>  
F;127-167/Domain: NGF receptor repeat homology <NG3>  
F;168-196/Domain: NGF receptor repeat homology <NG4>  
F;212-234/Domain: transmembrane #status predicted <MEM>  
F;235-455/Domain: intracellular #status predicted <INT>  
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 18.5%; Score 201.5; DB 1; Length 455;  
Best Local Similarity 30.6%; Pred. No. 5e-08;  
Matches 49; Conservative 21; Mismatches 73; Indels 17; Gaps 5;  
QY 23 LLLLLLLLLPLQV-----KFALELHSPKCPAGEY---WSKDVCKKCSAGTFV 69  
DB 9 LLLPLVLELVGLVPSGVTGLVPHLGDRKRDVSPQGYIHPQNNISCTCKHKGTYL 68  
QY 70 KAPCEIPTQGCCKHPGFTTEKDNLYLDACILCTCDKD--QEMVADCSATSDRKQCQR 127  
DB 69 YNDCPGQQTDCRECSGSFTASENHLRCLSCSKCKEMGQVEISSCTVDRDVTVCGR 128  
QY 128 TGLY-YDPRFPSCRCCTKCPQIGPVLQECNSTANTVCS 166  
DB 129 KQVRYHWSNLFQCFNCSICLNG-TVHLSCQEKQNTVCT 167  
RESULT 9  
JC4302  
tumor necrosis factor receptor p55 precursor - pig  
C;Species: Sus scrofa domestica (domestic pig)  
C;Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
C;Accession: JC4302; PC4093  
R;Suter, B.; Faull, U.  
Gene 163, 263-266, 1995  
A;Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
A;Reference number: JC4302; MUID:96011645; PMID:7590278  
A;Accession: JC4302  
A;Molecule type: mRNA  
A;Residues: 1-461 <SUT>  
A;Cross-references: UNIPROT:P50555; GB:U19994; NID:gl1141752; PIDN:AAC48499.1; PID:gl11417  
A;Accession: PC4093  
A;Molecule type: protein  
A;Residues: 1-7 <SU2>  
A;Experimental source: kidney cell line 15  
C;Genetics:  
A;Gene: tnfr  
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolog  
C;Keywords: glycoprotein; kidney; receptor; transmembrane protein; tumor  
F;1-29/Domain: signal sequence #status predicted <SIG>  
F;30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
F;44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
F;84-126/Domain: NGF receptor repeat homology <NG1>  
F;84-126/Domain: NGF receptor repeat homology <NGF>  
F;211-231/Domain: transmembrane #status predicted <TMW>  
F;361-447/Domain: signal transduction #status predicted <SIT>  
F;54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
Query Match 18.4%; Score 200.5; DB 2; Length 461;

Best Local Similarity 30.8%; Pred. No. 6e-08;  
Matches 49; Conservative 25; Mismatches 70; Indels 15; Gaps 7;  
QY 21 LLLLLLLLLLNLN-PLQKFAML-----ELHSPKCPAGEY---WSKDVCKKCSAGTFVKA 71  
DB 11 LPLVLRALLVDVYPAGVHGLVHPGDKREKRESICPOGKYSHPNRSICCTCKCHKGIYLNH 70  
QY 72 PCBIPHTQGCCKHPGFTTEKDNLYLDACILCTC--DKDQEMVADCSATSDRKQCQR 129  
DB 71 DCLGPGGLDTCRECDNGTFTASENHLTCLCSCKRSEMSQVBISPTVDRDVTVCGRKN 130  
QY 130 LY--YDPRFPSCRCCTKCPQIGPVLQECNSTANTVCS 166  
DB 131 QVRKYWSETLQ-CLNCSICLCPNG-TVOLPCLEKQDTICN 167  
RESULT 10  
QGHUN  
nerve growth factor receptor precursor, low affinity [validated] - human  
N;Alternate names: NGF receptor  
C;Species: Homo sapiens (man)  
C;Date: 31-Mar-1988 #sequence\_revision 31-Mar-1988 #text\_change 09-Jul-2004  
C;Accession: A25218; A60204; S21689; I57638  
R;Johnson, D.; Ianahan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.  
Cell 47, 545-554, 1986  
A;Title: Expression and structure of the human NGF receptor.  
A;Reference number: A25218; MUID:87051725; PMID:3022937  
A;Accession: A25218  
A;Molecule type: mRNA  
A;Residues: 1-427 <JOH>  
A;Cross-references: UNIPROT:P08138; GB:M14764; NID:gi189204; PIDN:AAB59544.1; PID:gi189205  
R;Marano, N.; Dietzschold, B.; Barley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;  
J. Neurochem. 48, 225-232, 1987  
A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factor  
A;Reference number: A60204; MUID:87085574; PMID:3025363  
A;Accession: A60204  
A;Molecule type: protein  
A;Residues: 29-31,'T',33-42,'TT',45-46,'TX',50-51,'XX',54-56 <MAR>  
A;Experimental source: melanoma cell line A875  
A;Note: This sequence has been corrected by a note added in proof to follow the nucleotide  
R;Vissavajjhala, P.; Leszyk, J.D.; Lin-Goerke, J.; Ross, A.H.  
Arch. Biochem. Biophys. 294, 244-252, 1992  
A;Title: Structural domains of the extracellular domain of human nerve growth factor rec  
A;Reference number: S21689; MUID:92198017; PMID:1372492  
A;Accession: S21689  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 183-208 <VIS>  
R;Sehgal, A.; Patil, N.; Chao, M.  
Mol. Cell. Biol. 8, 3160-3167, 1988  
A;Title: A constitutive promoter directs expression of the nerve growth factor receptor  
A;Reference number: I57638; MUID:89096903; PMID:2850481  
A;Accession: I57638  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: DNA  
A;Residues: 1-22 <RES>  
A;Cross-references: GB:M21621; NID:gi189206; PIDN:AAA36363.1; PID:gi189207  
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C;Comment: This protein is thought to form a high-affinity receptor when it associates w  
C;Comment: This receptor undergoes both N- and O-linked glycosylation.  
C;Genetics:  
A;Gene: GDB:NGFR  
A;Cross-references: GDB:120234; OMIM:162010  
A;Map position: 17q21-17q22  
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t  
F;1-28/Domain: signal sequence #status predicted <SIG>  
F;29-427/Product: nerve growth factor receptor #status predicted <MAT>  
F;29-250/Domain: extracellular #status predicted <EXT>  
F;32-65/Domain: NGF receptor repeat homology <NG1>  
F;67-108/Domain: NGF receptor repeat homology <NG2>  
F;109-147/Domain: NGF receptor repeat homology <NG3>

F:149-189/Domain: NGF receptor repeat homology <NG4>  
F:197-248/Region: serine/threonine-rich  
F:251-272/Domain: transmembrane #status predicted <TRM>  
F:273-427/Domain: intracellular #status predicted <INT>  
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 17.3%; Score 188; DB 1; Length 427;  
Best Local Similarity 34.7%; Pred. No. 4.9e-07;  
Matches 50; Conservative 11; Mismatches 69; Indels 14; Gaps 5;

Qy 24 LLLLLLLNLPL-QVKFAMLELHSPKCPAGEYWSKDVCKNCSAGTFVKAPCEIPHTQOC 82  
Db LLLLLLLGVSLGGAKEA-----CPTGLYTHSGECKACNLGEGVAQPCGA--NQTV 64

Qy 83 EKCHPG-TFTSEKDNVLDALICSTCDKQDMVADCSATSDRKQCRTGLYYDDPKFPESC 141  
Db EPLCDSVTFSDVWATEPKCTECVGLQSMSPAPCVADDAVCRCAYG--YYQDETTRGC 122

Qy 142 RPTCKCPGIPVLQECNSTANTVC 165  
Db 123 EACRVCERAGSLVFSQDKQNTVC 146

RESULT 11  
S12783

OX40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homology  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C:Accession: S12783; S08036  
R:Mallett, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990

A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte  
A:Reference number: S12783; MUID:90214614; PMID:2157591  
A:Accession: S12783  
A:Molecule type: mRNA  
A:Residues: 1-271 <MAL>  
A:Cross-references: UNIPROT:P15725; EMBL:X17037; NID:G57830; PIDN:CAA34897.1; PID:G57831  
C:Superfamily: CD27 antigen; NGF receptor repeat homology  
C:Keywords: growth factor receptor; transmembrane protein  
F:1-19/Domain: signal sequence #status predicted <SIG>  
F:20-271/Product: OX40 antigen #status predicted <SIG>  
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 17.2%; Score 186.5; DB 2; Length 271;  
Best Local Similarity 27.1%; Pred. No. 4.5e-07;  
Matches 51; Conservative 27; Mismatches 71; Indels 39; Gaps 8;

Qy 16 FLWRRLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVCKNCSAGTFVKAPCEI 75  
Db 2 YVWVQPTAFLLGLSLGVTK-----LNCVKDTYPSGHKCRQCQPGHGWSRCD- 52

Qy 76 PHTQGG-CEKCHPGTFTSEKDNVLDALICSTCD--KQDMVADCSATSDRKQCRTGLY- 131  
Db 53 -HTRDTVCHPCPGFYNAVNY-DTCQCTQCNHRSGSELKQNTPTEDTVCCQCPGTQP 110

Qy 132 -----YDPKFPESCRTCKP-QGIPVLQECNSTANTVCSSVSNP 172  
Db 111 QDSSHLGLGVDCVPCPPGHFSGNQACKPWTNCTLSGKQIRHPASNSLDTVCED----- 165

Qy 173 RNRLLPLLL 180  
Db 166 RSLLATLL 173

RESULT 12  
A40036

N:Alternate names: surface antigen Fas precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 09-Jul-2004  
C:Accession: A40036; S24543; A38142  
R:Itoh, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, S.I.; Sameshima, M.; Hase,

Cell 66, 233-243, 1991  
A:Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can m  
A:Reference number: A40036; MUID:91309137; PMID:1713127  
A:Accession: A40036  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-335 <ITO>  
A:Cross-references: UNIPROT:P25445; GB:M67454; NID:G182409; PIDN:AAA63174.1; PID:G182  
R:Kramer, P.H.  
submitted to the EMBL Data Library, February 1992  
A:Reference number: S24543  
A:Accession: S24543  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-335 <KRA>  
A:Cross-references: EMBL:X63717; NID:G28741; PID:G28742  
R:Oehm, A.; Behrmann, I.; Falk, W.; Pawlita, M.; Maier, G.; Klas, C.; Li-Weber, M.; R  
J. Biol. Chem. 267, 10709-10715, 1992  
A:Title: Purification and molecular cloning of the APO-1 cell surface antigen, a membe  
A:Reference number: A38142; MUID:92268122; PMID:1375228  
A:Accession: A38142  
A:Status: preliminary; not compared with conceptual translation  
A:Molecule type: nucleic acid  
A:Residues: 1-134, 'Q', 136-335 <OEH>  
A:Experimental source: SKM6.4 cells  
A:Note: sequence extracted from NCBI backbone (NCBIP:103810)  
C:Genetics:  
A:Gene: GDB:APT1  
A:Cross-references: GDB:132671; OMIM:134637  
A:Map position: 10q24.1-10q24.1  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat hom  
C:Keywords: apoptosis; surface antigen; transmembrane protein  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:85-128/Domain: NGF receptor repeat homology <NG4>  
F:174-190/Domain: transmembrane #status predicted <TM>

Query Match 16.9%; Score 183.5; DB 2; Length 335;  
Best Local Similarity 30.8%; Pred. No. 8.9e-07;  
Matches 41; Conservative 23; Mismatches 62; Indels 7; Gaps 5;

Qy 59 CCKNCSAGTFVKAPCEIPHTQOCCKCHPG-TFTSEKDNVLDALICSTCDKQ--EMVAD 115  
Db 59 CHKPCPGERKARDCTVNGDEPDCVPCQEGKEYTDKAHFKSKCRCLCDGEGHLEVEIN 118

Qy 116 CSATSDRKQCRTGLYYDDPKFPESCRTCKPQGIPLVQECNSTANTVCSSVSNP-N 174  
Db 119 CTRTQNTKCRKPN-PFCNSTVCEHCDPCTKCEHGI--IKECTLTSTKCKEGSRNLG 175

Qy 175 RLFLLLSPLSVLI 187  
Db 176 WLCLLLPLIPLIV 188

RESULT 13  
JC7705

death receptor-6 - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Jul-2004  
C:Accession: JC7705  
R:Brigham, J.T.; Bohe, J.; Goetz, F.W.; Johnson, A.L.  
Biochem. Biophys. Res. Commun. 284, 1109-1115, 2001  
A:Title: Conservation of death receptor-6 in avian and piscine vertebrates.  
A:Reference number: JC7705; MUID:21308433; PMID:11414698  
A:Accession: JC7705  
A:Molecule type: mRNA  
A:Residues: 1-651 <BRI>  
A:Cross-references: UNIPROT:Q98SM6; GB:AF349908  
C:Comment: This receptor, a member of the tumor necrosis factor receptor family, belo  
tresa, activates a cell death and/or survival signaling cascade.  
C:Genetics:  
A:Gene: dr-6  
C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat hom

C;Keywords: ovary  
F;1-21/Domain: signal sequence #status predicted <SIG>  
F;52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>  
F;332-350/Domain: transmembrane #status predicted <TM>  
F;410-475/Domain: death domain #status predicted <DED>  
F;551-651/Region: conserved cytoplasmic #status predicted

Query Match 16.6%; Score 180.5; DB 2; Length 651;  
Best Local Similarity 29.8%; Pred. No. 2.4e-06;  
Matches 45; Conservative 27; Mismatches 66; Indels 13; Gaps 5;

Qy 22 LLLLLLLLPLOVKFAMLELHSPKCPAGRY-----WSKDVCKKNCAGTFVKAPCEI 75  
Db 9 VLPLVLFGTADAPKLTLS-EQNVSILPAGKYLHLDRATNQELICDKCPAGTYVSKHC-T 66  
Qy 76 PHTQCEKCHPGFTFKDKNYLDACILC-STCDKQDMVADCSATSDRKCOCRTGLYYD 134  
Db 67 KSTLRECSPCPDGFTFKHENGIERCHPCPKCPCLPMIEKTHCTALTDRCTCLSGTF--- 123  
Qy 135 KPFPESCRCPTKCPQGIPLVQECNSTANTVC 165  
Db 124 -QINDTCVPYTVCPVGMGVRKKGTFETEDVRC 153

## RESULT 14

JN0006  
nerve growth factor receptor, low affinity precursor - chicken  
N;Alternate names: NGF receptor  
C;Species: Gallus gallus (chicken)  
C;Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 09-Jul-2004  
C;Accession: JN0006; A60504  
R;Large, T.H.; Weiskamp, G.; Heider, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid  
Neuron 2, 1123-1134, 1989  
A;Title: Structure and developmental expression of the nerve growth factor receptor in b  
A;Reference number: JN0006; MUID:90166579; PMID:2560385  
A;Accession: JN0006  
A;Molecule type: mRNA  
A;Residues: 1-416 <LAR>  
A;Cross-references: UNIPROT:P18519  
A;Experimental source: embryonic chick brain  
R;Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, B.F.; Bothwell, M.  
Dev. Biol. 137, 287-304, 1990  
A;Title: Structure and developmental expression of the chicken NGF receptor.  
A;Reference number: A60504; MUID:90152140; PMID:2154393  
A;Accession: A60504  
A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA  
A;Residues: 21-35, 'Y', 37-172, 'K', 174-275, 'S', 277-395, 'R', 397-416 <HEU>  
C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c  
C;Comment: The cysteine-rich region of the extracellular domain may form part or all of  
C;Comment: This protein is thought to form a high-affinity receptor when it associates w  
C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology  
C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; b  
F;1-20/Domain: signal sequence #status predicted <SIG>  
F;21-416/Product: nerve growth factor receptor #status predicted <MAT>  
F;21-239/Domain: extracellular #status predicted <EXT>  
F;24-57/Domain: NGF receptor repeat homology <NG1>  
F;59-100/Domain: NGF receptor repeat homology <NG2>  
F;101-139/Domain: NGF receptor repeat homology <NG3>  
F;141-181/Domain: NGF receptor repeat homology <NG4>  
F;189-237/Region: serine/threonine-rich  
F;240-261/Domain: transmembrane #status predicted <MEM>  
F;262-416/Domain: intracellular #status predicted <INT>  
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 16.2%; Score 176.5; DB 1; Length 416;  
Best Local Similarity 30.7%; Pred. No. 3.4e-06;  
Matches 43; Conservative 20; Mismatches 68; Indels 9; Gaps 4;

Qy 27 LLLLLLPLOVKFAMLELHSPKCPAGRYWSKDVCKKNCAGTFVKAPCEIHTQCEKCH 86  
Db 7 LLLLLLPAGTWSKE-----KLTFTMTTSGECCCKACNLGEGVQPCGV--NQTVCPECL 60

Qy 87 PG-TFTEKONYLDACILCSTCDKQDMVADCSATSDRKCOCRTGLYYDPKFPESCRCPT 145  
Db 61 DSVTYSDTVSATPCKPCKPCTQCVGLHSMSPAPCVESDDAVCRCAYG--YFQDELSCGCKECS 118  
Qy 146 KCPQGIPLVQECNSTANTVC 165  
Db 119 ICEVGFGLMPFPCRSQDTVC 138

## RESULT 15

I37383  
FAS soluble protein - human  
C;Species: Homo sapiens (man)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I37383  
R;Cascino, I.; Ficuci, G.; Papoff, G.; Ruberti, G.  
J. Immunol. 154, 2706-2713, 1995  
A;Title: Three functional soluble forms of the human apoptosis-inducing Fas molecule are  
A;Reference number: I37383; MUID:95181785; PMID:7533181  
A;Accession: I37383  
A;Status: preliminary; translated from GB/EMBL/DBJ  
A;Molecule type: mRNA  
A;Residues: 1-314 <RES>  
A;Cross-references: UNIPROT:P25445; EMBL:Z47993; NID:9728578; PIDN:CAA88031.1; PID:96955  
C;Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homolo

Query Match 16.1%; Score 175; DB 2; Length 314;  
Best Local Similarity 31.6%; Pred. No. 3.6e-06;  
Matches 36; Conservative 19; Mismatches 53; Indels 6; Gaps 4;

Qy 59 CCNCSAGTFVKAPCEIPIHTQCEKCHPG-TFTEKONYLDACILCSTCDKQ--EMVAD 115  
Db 59 CHKPCPPGERKARDCTVNGDEPDVCPQCEGKYTDKAHFSKCRRCRLCDEGHGLEVIN 118  
Qy 116 CSATSDRKCOCRTGLYYDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSV 169  
Db 119 CTRTQNTKCRKN-PFCNSTVCEHCDCPTKCEHGI--IKECTLTSNTKKEEV 169

Search completed: September 9, 2005, 09:31:38  
Job time : 144.524 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 8, 2005, 23:31:32 ; Search time 740.143 Seconds  
(without alignments)  
136.989 Million cell updates/sec

Title: US-10-622-407-8

Perfect score: 1087

Sequence: 1 MFGFFCSLVSLSRWFLWRR.....LLSPLSLVSVVVFRIIRR 198

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1087	100.0	198	1	TR22 MOUSE
2	746.5	68.7	176	1	TR23 MOUSE
3	320	29.4	204	1	TR26 MOUSE
4	303	27.9	438	2	Q9DFV0
5	286.5	26.4	225	2	Q7T3M7
6	286.5	26.4	410	2	Q7T3M8
7	284.5	26.2	395	2	Q800K8
8	280	25.8	357	2	Q9DFJ4
9	265.5	24.4	321	2	Q6DJ81
10	247	22.7	328	2	Q76B99
11	246	22.6	328	2	Q6GLZ4
12	243.5	22.4	327	2	Q97491
13	239.5	22.0	289	2	Q678B7
14	239	22.0	189	2	Q95185
15	233	21.4	323	1	TNR6 BOVIN
16	233	21.4	446	2	Q95ND3
17	232	21.3	328	2	Q76B98
18	226	20.8	440	2	Q6QHF0
19	226	20.8	440	2	Q6QHF1
20	226	20.8	454	1	TR1A MOUSE
21	224.5	20.7	332	1	TNR6 PIG
22	224	20.6	319	2	Q9TV79
23	223	20.5	440	2	Q6QHF2
24	221	20.3	347	2	Q57119
25	218.5	20.1	263	2	Q9XS60
26	218.5	20.1	320	2	Q9XS29
27	218.5	20.1	327	1	TNR6 MOUSE
28	216	19.9	189	2	Q97530
29	216	19.9	360	2	Q57118
30	215.5	19.8	326	2	Q57120
31	215.5	19.8	348	2	O57103

32	215.5	19.8	348	2	O57108
33	215.5	19.8	348	2	O57277
34	215.5	19.8	349	2	O57101
35	215.5	19.8	349	2	O57102
36	215.5	19.8	349	2	O57291
37	215.5	19.8	349	2	O57305
38	215.5	19.8	349	2	O57305
39	213.5	19.6	351	2	O57121
40	213.5	19.6	351	2	O6WB14
41	213.5	19.6	351	2	O57122
42	212.5	19.5	349	2	CRMB COMPX
43	212.5	19.5	389	2	O57099
44	212.5	19.5	461	1	Q6NUU6
45	211.5	19.5	318	2	TR1A RAT
					Q7T2H3

#### ALIGNMENTS

#### RESULT 1

ID	TR22_MOUSE	STANDARD;	PRT;	198 AA.
AC	Q9ER62; Q8VHB9; Q9CZ44;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 22 (Tumor necrosis factor receptor p60 homolog 2) (TNF receptor family member SOBa)			
DE	(Decoy TRAIL receptor 2) (TNF receptor homolog 2)			
GN	Name=Tnftrsf22; Synonyms=Dctrailr2, Tnftrh2, Tnftrsf1a2;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	STRAIN=129/Sv; TISSUE=Embryonic stem cells;			
RX	MEDLINE=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691;			
RA	Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,			
RA	Lane N., Reik W., Walter J.;			
RT	"Sequence and functional comparison in the Beckwith-Wiedemann region: implications for a novel imprinting centre and extended imprinting.";			
RL	Hum. Mol. Genet. 9:2691-2706(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND 3D-STRUCTURE			
RP	MODELING OF 62-170.			
RC	STRAIN=NIH Swiss;			
RX	PubMed=12465268; DOI=10.1074/jbc.M210783200;			
RA	Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A.,			
RA	Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,			
RA	Burkly L.C., Tschopp J., Zheng T.S.;			
RT	"Identification of a new murine tumor necrosis factor receptor locus that contains two novel murine receptors for tumor necrosis factor-related apoptosis-inducing ligand (TRAIL).";			
RL	J. Biol. Chem. 278:5444-5454(2003).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RC	Risser P., Mao W., Baldwin D.T., Pan G.;			
RA	"Characterization of SOBa, a murine member of the TNFR family.";			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	STRAIN=C57BL/6J; TISSUE=Embryo;			
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;			
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojibori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schraml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,			
RA	Blake J.A., Bratt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,			
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,			
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,			

O57108	monkeypox v
O57277	monkeypox v
O57101	monkeypox v
O57102	monkeypox v
O57291	monkeypox v
O57305	cowpox viru
O57121	cowpox viru
O6WB14	callithrix
O57122	cowpox viru
O73559	cowpox viru
O6NUU6	brachydanio
P22934	rattus norv
Q7T2H3	oncorhynchus

RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,  
RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,  
RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,  
RA Nagashima T., Numata K., Okido T., Pavan W.J., Perte G., Pesole G.,  
RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,  
RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,  
RA Sadelin A., Schneider C., Semple C.A., Setou M., Shimada K.,  
RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,  
RA Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,  
RA Wilming L.G., Wyszynski-Boris A., Yanagisawa M., Yang I., Yang L.,  
RA Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,  
RA Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,  
RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,  
RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,  
RA Yaeunishi A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,  
RA Yashunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,  
RA Birney E., Hayashizaki Y.,  
RA "Analysis of the mouse transcriptome based on functional annotation of  
RT 60,770 full-length cDNAs";  
RL Nature 420:563-573 (2002).  
CC -!- FUNCTION: Receptor for the cytotoxic ligand TNFSF10/TRAIL. Lacks a  
CC cytoplasmic death domain and hence is not capable of inducing  
CC apoptosis. Protects cells against TRAIL mediated apoptosis  
CC possibly through ligand competition. Cannot induce the NF-kappa-B  
CC pathway.  
CC -!- SUBCELLULAR LOCATION: Type II membrane protein (isoform 1);  
CC secreted (isoform 2) (Potential).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1;  
CC IsoId=Q9ER62-1; Sequence=Displayed;  
CC Name=2;  
CC IsoId=Q9ER62-2; Sequence=VSP\_007648;  
CC -!- TISSUE SPECIFICITY: Ubiquitous.  
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.  
CC -!- CAUTION: Ref.1 (CAC27353) sequence differs from that shown due to  
CC erroneous gene model prediction.  
CC -!- CAUTION: Ref.1 (CAC16406) sequence differs from that shown due to  
CC a frameshift in position 38.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AJ278265; CAC16406.1; ALT\_FRAME.  
DR EMBL; AJ276505; CAC27353.1; ALT\_SEQ.  
DR EMBL; AY165626; AAN87806.1; -.  
DR EMBL; AY165627; AAN87807.1; -.  
DR EMBL; AY046551; AAL05073.1; -.  
DR EMBL; AK012838; BAB28502.2; ALT\_INIT.  
DR HSP; Q92956; IJWA.  
DR MGB; MG1:1930270; Tnfref22.  
DR GO; GO:0016021; C:integral to membrane; NAS.  
DR GO; GO:0004872; F:receptor activity; IDA.  
DR GO; GO:0045569; F:TRAIL binding; IDA.  
DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.  
DR GO; GO:0042981; F:regulation of apoptosis; IDA.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 3.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.  
DR PROSITE; PS00500; TNFR\_NGFR\_2; 2.  
KW Alternative splicing; Glycoprotein; Receptor; Repeat; Signal-anchor;  
KW Transmembrane.  
FT DOMAIN 1 20 Cytoplasmic (Potential).  
FT SIGNAL 21 41 Signal-anchor for type II membrane  
FT TRANSMEM 21 41 protein (Potential).  
FT FT FT  
FT DOMAIN 42 198 Extracellular (Potential).  
FT REPEAT 47 82 TNFR-Cys 1.

FT REPEAT 84 124 TNFR-Cys 2.  
FT REPEAT 125 165 TNFR-Cys 3.  
FT DISULFID 48 59 By similarity.  
FT DISULFID 60 73 By similarity.  
FT DISULFID 63 82 By similarity.  
FT DISULFID 85 100 By similarity.  
FT DISULFID 103 116 By similarity.  
FT DISULFID 106 124 By similarity.  
FT DISULFID 126 141 By similarity.  
FT DISULFID 144 157 By similarity.  
FT DISULFID 147 165 By similarity.  
FT CARBOHYD 62 62 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 158 158 N-linked (GlcNAc...) (Potential).  
FT VARSPLIC 171 198 NPNRFLLSPLSLVSVLVVVFRIIR -> RRSASVAMP  
FT I (in isoform 2).  
FT /FTID=VSP\_007648.  
FT L -> V (in Ref. 2).  
FT L -> C (in Ref. 1; CAC16406).  
FT LALL -> CVV (in Ref. 1; CAC16406).  
SQ SEQUENCE 198 AA; 22375 MW; EBF8F52961EA9983 CRC64;  
Query Match 100.0%; Score 1087; DB 1; Length 198;  
Best Local Similarity 100.0%; Pred. No. 3.4e-85;  
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLNLPLQVKFAMLEHSPKCPAGEYWSKDVCC 60  
Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLNLPLQVKFAMLEHSPKCPAGEYWSKDVCC 60  
Qy 61 KNCAGTFVKAPEIPHTQGCCKHPGTFTEKDYNDACILGTCSTCDKDEWADCSATS 120  
Db 61 KNCAGTFVKAPEIPHTQGCCKHPGTFTEKDYNDACILGTCSTCDKDEWADCSATS 120  
Qy 121 DRKQCRTGLYYDPKPPESCPCCTKCPQGPVLQECNSTANTVTVSSSVNPNRNLFLLL 180  
Db 121 DRKQCRTGLYYDPKPPESCPCCTKCPQGPVLQECNSTANTVTVSSSVNPNRNLFLLL 180  
Qy 181 SPLSLVSVLVVVFRIIR 198  
Db 181 SPLSLVSVLVVVFRIIR 198  
RESULT 2  
TR23\_MOUSE STANDARD; PRT; 176 AA.  
AC Q9ER63; Q8VHC0;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 23 precursor (Tumor  
DE necrosis factor receptor p60 homolog 1) (TNF receptor family member  
DE SOB) (Decoy TRAIL receptor 1) (TNF receptor homolog 1).  
GN Name=Tnf:rsf23; Synonyms=Dctrailr1, Tnf:rl, Tnf:rsf1all;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=129/SV; TISSUE=Embryonic stem cells;  
RX MEDLINE=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691;  
RA Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,  
RA Lane N., Reik W., Walter J.;  
RA "Sequence and functional comparison in the Beckwith-Wiedemann region:  
RA implications for a novel imprinting centre and extended imprinting";  
RL Hum. Mol. Genet. 9:2691-2706 (2000).  
RN [2]  
RP SEQUENCE FROM N.A.; FUNCTION, SUBCELLULAR LOCATION, AND 3D-STRUCTURE  
RP MODELING OF 52-160.  
RX STRAIN=C57BL/6;  
RX PubMed=1246268; DOI=10.1074/jbc.M210783200;  
RA Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A.,  
RA Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,



FT	DISULFID	126	143		By similarity.
FT	CARBOHYD	57	57		N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	136	136		N-linked (GlcNAc. .) (Potential).
SQ	SEQUENCE	204 AA;	22708 MW;	A35C5177F178C3DD CRC64;	
 Query Match            29.4%; Score 320; DB 1; Length 204; Best Local Similarity 37.9%; Pred. NO. 1.3e-19; Matches 67; Conservative 31; Mismatches 71; Indels 8; Gaps 5;					
Qy	24	L L L L L L N L P Q V K F A M E L H S F K - C P A G E Y W S K D V C K C N G S A G T F V K A P C E I P H T Q S C	82		
Dd	4	L R L L L L G L L U R V - A V C S V N T I L K I G E F K H N L C L Q C S A G T Y L R N P C Q E N H N S E C	61		
Qy	83	E K C H P G T F T K O N Y L D A C I L G S T C D Q E M W A D C S A T S D R K C Q C R T G L Y Y Y D P K P P S C R	142		
Dd	62	A P C D S E H F I D H K N R E S E C F P C S C R D D Q E E V A K C S R T A D R V C Q K Q G T C D S E N C L E R C H	121		
Qy	143	P T Y K C P G I P V Q B C N S T A N T V C S S V S N P - - - R N R L F L L S P L S V L I V S V V F R I I	196		
Dd	122	T C S S C P D G - R Y V R K C N A T M D T V C D K F D S E P Q G S Q C F C F S K P L G I V V I - I A A F I I I	176		
 RESULT 4					
ID	Q9DFV0			PRELIMINARY;	PRT; 438 AA.
AC	Q9DFV0;				
DT	01-MAR-2001	(TrEMBLrel. 16, Created)			
DT	01-MAR-2001	(TrEMBLrel. 16, Last sequence update)			
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)			
DE	Ovarian TNF receptor.				
GN	Name=tnfrsf1a;				
OS	Brachydanio rerio (Zebrafish) (Danio rerio).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;				
OC	Cyprinidae; Danio.				
OX	NCBI_TaxId=7955;				
RX	[1]				
RA	SEQUENCE FROM N.A.				
RP	Boe J., Goetz F.W.				
RF	"Molecular cloning and expression of a TNF receptor and two TNF				
RT	ligands in the fish ovary."				
RL	Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481 (2001).				
DR	EWBL; AF250042; AAG24365.1; -. HSP; Q92956; IQWA.				
DR	ZFN; ZDB-GENE-010802-1; tnfrsf1a.				
DR	GO; GO:0005515; F:protein binding; IEA.				
DR	GO; GO:0004872; F:receptor activity; IEA.				
DR	GO; GO:0007185; P:signal transduction; IEA.				
DR	InterPro; IPRO00345; CytC_heme_BS.				
DR	InterPro; IPRO11029; DEATH like.				
DR	InterPro; IPRO01368; TNFR_C6.				
DR	Pfam; PF00531; Death; 1.				
DR	Pfam; PF00020; TNFR_c6; 2.				
DR	SMART; SM00208; TNFR; 3.				
DR	PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.				
DR	PROSITE; PS0017; DEATH DOMAIN; 1.				
DR	PROSITE; PS00652; TNFR_NGPR_1; 1.				
DR	PROSITE; PS0050; TNFR_NGPR_2; 2.				
KW	Receptor.				
SQ	SEQUENCE	438 AA;	49103 MW;	B7E5312BB6E80B04 CRC64;	

[illegible]

Qy	161	ANTWC-----SSSVSNPRNRLFLLLSPLSVLIVSVVVFRII 196
		:    :    :    :
Db	158	SNTRCRRRPSYPTGPTKPSASNSTGTIFVIVSILILLVCTIVGAIL 206
		:    :    :    :
RESULT 5		
Q7T3M7		PRELIMINARY; PRT; 225 AA.
AC	Q7T3M7	
DT	01-OCT-2003	(TREMBLrel. 25, Created)
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)
DE	Death domain-containing tumor necrosis factor receptor superfamily member 23 variant 2.	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	
OX	NCBI_TaxID=9031;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	PubMed=14645108;	
RA	Bridgham J.T., Johnson A.L.;	
RT	"Alternatively spliced variants of Gallus gallus TNFRSF23 are expressed in the ovary and differentially regulated by cell signaling pathways.";	
RL	Biol. Reprod. 70:972-979(2004).	
DR	EMBL; AY251409; AAP41834.1; -.	
DR	HSP; O14763; 1DU3.	
DR	GO; GO:0004872; F:receptor activity; IEA.	
DR	InterPro; IPR001450; 4Fe4S_ferredoxin.	
DR	InterPro; IPR006209; EGF-like.	
DR	InterPro; IPR001368; TNFR_c6.	
DR	Pfam; PF00020; TNFR_c6; 3.	
DR	SMART; SM00208; TNFR; 3.	
DR	PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.	
DR	PROSITE; PS01186; EGF_2; UNKNOWN_1.	
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.	
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.	
KW	Receptor.	
SQ	SEQUENCE 225 AA; 24697 MW; 59FC9C0AE4530630 CRC64;	
Query Match 26.4%; Score 286.5; DB 2; Length 225;		
Best Local Similarity 39.6%; Pred. No. le-16; Mismatches 53; Indels 11; Gaps 5;		
Matches 59; Conservative 26;		
Qy	19	RLRLRLRLRLRLPLQVKFAMLLHSPKCPAGEYWSKDVCCKNCAGTFVKAPCEIPT 78
		:    :    :    :    :    :    :
Db	4	RAVGLLLLVTLTVP----GSKAEV----CGEGEYLXEDICMLCPAGTYVAQHCRIFHS 55
		:    :    :    :    :    :    :
Qy	79	OGQCEKCHPG-TTFEKONYLDACILCSTCDKQEWADCSATSRKCCOCTGLYYIDPKF 137
		:    :    :    :    :    :    :
Db	56	RKCASTCEGRDYTAHANGLEECILCRQKDDQITLRTCTVTSDTECOCHQG-YFCPAEG 114
		:    :    :    :    :    :    :
Qy	138	PESCRPTK-CQGIPIVLQECNSTANTVC 165
		:    :    :    :    :    :    :
Db	115	CEICQRTCTCPGREGREIVQICNATMDLGC 143
		:    :    :    :    :    :    :
RESULT 6		
Q7T3M8		PRELIMINARY; PRT; 410 AA.
AC	Q7T3M8	
DT	01-OCT-2003	(TREMBLrel. 25, Created)
DT	01-OCT-2003	(TREMBLrel. 25, Last sequence update)
DT	01-MAR-2004	(TREMBLrel. 26, Last annotation update)
DE	Death domain-containing tumor necrosis factor receptor superfamily member 23 variant 1 (Fragment).	
OS	Gallus gallus (Chicken).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;	
OC	Gallus.	

DR	InterPro; IPRO00488; Death.
DR	InterPro; IPRO11029; DEATH_like.
DR	InterPro; IPRO01368; TNFR_C6.
DR	InterPro; IPRO01878; Znf_CCHC.
DR	Pfam; PF00531; Death; 1.
DR	Pfam; PF00020; TNFR_c6; 2.
DR	SMART; SM00208; TNFR; 3.
DR	SMART; SM00343; Znf_C2HC; 2.
DR	PROSITE; PS00017; DEATH_DOMAIN; 1.
DR	PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR	PROSITE; PS00050; TNFR_NGFR_2; 2.
KW	Receptor.
SQ	SEQUENCE 395 AA; 44304 MW; 8D685A9F74710AE1 CRC64;

  

Query Match	26.2%; Score 284.5; DB 2; Length 395;
Best Local Similarity	33.2%; Pred. No. 2.6e-16;
Matches 61; Conservative 32; Mismatches 84; Indels 7; Gaps 2;	

  

Qy	20 RLLLLLLLLLNLIP-LQVRFAMLELHSFKCPAGEYMSKDVCKNCNSAGTFVKAPCEIPT 78
Dd	9 RLVLVLLSSGVFPQGRIDFRGTQRDLCSNDQNYLGNNCCLNPCAGTHVKGHCKSKSGE 68
Qy	79 QGOCEKCHPCTFEKXNLYLDACILSCDCKDQBWADCSATSDRKCCORTGLYYYPDKFP 138
Dd	69 KGQCQECDYTYTAHPNELNQCFPTPCRDPQDIHVTPCLTQTQTECOCKAGRCDPHQAC 128
Qy	139 ESCRPTCKPGQIPVLQECNSTANTVC-----SSSVSNPNRFLFLLSPLSLIVSVV 192
Dd	129 EVCKKSKCEKDEIERNCTSTNTTECKTKPNSGSGASGNKDVIADVVPILGI VAVAV 188
Qy	193 FRII 196
Dd	189 AGVI 192

  

RESULT 8

Q9DF34

ID	Q9DF34	PRELIMINARY;	PRT;	357 AA.
AC	Q9DF34;			
DT	01-MAR-2001 (TrEMBLrel. 16, Created)			
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)			
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)			
DN	Death receptor.			
GE	Name=hdr;			
OS	Brachydanio rerio (zebrafish) (Danio rerio).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Cypriniformes;			
OC	Cyprinidae; Danio.			
OX	NCBI_TaxId=7955;			
RN	[1]			

SEQUENCE FROM N.A.

MEDLINE=20394298; PubMed=10934476; DOI=10.1038/35019592;

Long O., Huang H., Shafizadeh E., Liu N., Lin S.;

"Stimulation of erythropoiesis by inhibiting a new hematopoietic death

receptor in transgenic zebrafish."

Nat. Cell Biol. 2:549-552(2000).

DR EMBL; AF302789; AAG21396.1; -

DR HSP; Q92956; LUMA.

DR ZFIN; ZDB-GENE-030826-5; hdr.

DR GO; GO:0005515; F:protein binding; IEA.

DR GO; GO:0004872; F:receptor activity; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPRO00488; Death.

DR InterPro; IPRO11029; DEATH\_like.

DR InterPro; IPRO01368; TNFR\_C6.

DR Pfam; PF00531; Death; 1.

DR Pfam; PF00020; TNFR\_c6; 3.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00017; DEATH DOMAIN; 1.

DR PROSITE; PS00652; TNFR\_NGFR\_1; 3.

DR PROSITE; PS00050; TNFR\_NGFR\_2; 2.

KW Receptor.

SQ SEQUENCE 357 AA; 40662 MW; 1652B4840D9EEDBA CRC64;

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Query Match      25.8%; Score 280; DB 2; Length 357;
Best Local Similarity 32.4%; Pred. No. 5.8e-16;
Matches 61; Conservative 34; Mismatches 75; Indels 18; Gaps 4;

QY 20 RLLLLLLLLNL-----PQVKFAMLELHSPKCPAG-EYWSKDVCKKCSA 65
DB 2 RYIIVLLVLLLVNNAARSHGDLAWHRSVKRL--SRDVSRCRGLEYPHENICCLNCPA 59

QY 66 GTFVKAPCEIPHTQGCCKCHPGFTTEKDNLYDACILCSTCDKQDMVADCSATSDRKQC 125
DB 60 GTYVKKACAAAEKGVCAPECFDYTEHDHGLLKCIKCDKIDQETIEKCTSTQNTIRCK 119

QY 126 CRTGLYYDPKPPSPCRCTKCPGQIPVLQECNNTANTVC--SSSVNPNRNLFLLLSPL 183
DB 120 CRNGSFCLPDQACEVCKCKRCKDEETKSTAIKNTVCRKRNSPGSSTMTFTIVIMPL 179

QY 184 SVLIVSVV 191
DB 180 IVLLACVL 187

RESULT 9
ID Q6DJ81 PRELIMINARY; PRT; 321 AA.
AC Q6DJ81;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE MGC88957 protein.
GN Name=MGC88957;
OS Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8364;
RN [1];
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Shenmen C.M., Schuler G.D.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haehn F.,
RA Diatchenko L., Marubina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2];
RP SEQUENCE FROM N.A.
RC TISSUE=Whole body;
RA Klein S., Gerhard D.S.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075302; AAH75302.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR000345; CytC heme BS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.

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DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00198; 4FE4S FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00190; CYTOCHROME C; UNKNOWN_1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 321 AA; 36225 MW; 21E69219ABB34673 CRC64;

Query Match      24.4%; Score 265.5; DB 2; Length 321;
Best Local Similarity 34.0%; Pred. No. 9.1e-15;
Matches 65; Conservative 25; Mismatches 72; Indels 29; Gaps 5;

QY 4 FFGLSVLSRWFLRRLLLLLLLLNLPLQVKFAMLELHSPKCPAGEYWSKDVCKKNC 63
DB 8 FFC-----IFLLAAPTNGLPIS-----SDLY-----YQEGNIRCLRC 40

QY 64 SAGTFVKAPCEIPHTQGCCKCHPG-TFTEKDNLYDACILCSTCDKQDMVADCSATSDR 122
DB 41 PAGTFVEKPTKPTIGECSSCHTGSTYSEGTGLDHCLTCLRCRDDQEEVVRPCTATQNA 100

QY 123 KCCRTGLYYDPKPPSPCRCT-KCPQGIPLVQECNNTANTVCSSSVNPNRNLFLLLS 181
DB 101 ECRCKGTGTCPIDHPCPEVCLTCTCKPQGELOFPNCNSTSDSQGPAESGSWIVMLVLVL 160

QY 182 PLSVLIVSVV 192
DB 161 PLALLVLIVV 171

RESULT 10
Q76B99 PRELIMINARY; PRT; 328 AA.
ID Q76B99
AC Q76B99;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DB Death receptor-M1.
GN Name=xDR-M1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1];
RP SEQUENCE FROM N.A.
RX PubMed=14668340; DOI=10.1074/jbc.M306217200;
RA Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;
RT "Xenopus death receptor-M1 and -M2, new members of the tumor necrosis
factor receptor superfamily, trigger apoptotic signaling by
differential mechanisms.";
RL J. Biol. Chem. 279:7629-7635(2004).
DR EMBL; AB111446; BAB11770.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S ferredoxin.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4FE4S FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 328 AA; 37252 MW; 444D62A8ACBF9525 CRC64;

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Query Match      22.7%; Score 247; DB 2; Length 328;
Best Local Similarity 40.0%; Pred. No. 3.5e-13;
Matches 48; Conservative 21; Mismatches 49; Indels 2; Gaps 2;

QY 53 YWSKDVCCCKNSAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKONYLDACILCSTCDKQOE 111
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 38 YQAGNIRCLRCPCAGTVVEBCTTRDTKGECIPCHPGSTYSEGTGLDHLCLSCRCRDDQE 97
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 112 MVADCSATSDRKQOCRTGLYYDPKFPESCRCPTK-CPOGIPVLQECNSTANTVCSSTS 170
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 98 EVRSTCTATQNAECRCCKGTYCPMDHPCEVCLCTCTESCPGQELHLPNCNSTSDSHGCPAES 157
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 11
ID Q6GLZ4 PRELIMINARY; PRT; 328 AA.
AC Q6GLZ4;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE XDR-M1 protein.
GN Name=XDR-M1;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Datschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
initiative."
RL Dev. Dyn. 225:384-391(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Klein S., Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC074299; AAH74299.1;
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.

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DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00117; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 328 AA; 37262 MW; 7938B5F56F9C58E7 CRC64;

Query Match      22.6%; Score 246; DB 2; Length 328;
Best Local Similarity 40.0%; Pred. No. 4.3e-13;
Matches 48; Conservative 21; Mismatches 49; Indels 2; Gaps 2;

QY 53 YWSKDVCCCKNSAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKONYLDACILCSTCDKQOE 111
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 38 YQAGNIRCLRCPCAGTVVEBCTTRDTKGECIPCHPGSTYSEGTGLDHLCLSCRCRDDQE 97
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY 112 MVADCSATSDRKQOCRTGLYYDPKFPESCRCPTK-CPOGIPVLQECNSTANTVCSSTS 170
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 98 EVRPTCTATQNAECRCCKGTYCPMDHPCEVCLCTCTESCPGQELHLPNCNSTSDSHGCPAES 157
   |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 12
ID Q97491 PRELIMINARY; PRT; 327 AA.
AC Q97491;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Fas protein.
GN Name=Fas;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphocyte;
RA Takagi M., Takahashi H., Kabeya H., Ohashi K., Sugimoto C., Onuma M.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB011671; BAA37093.1;
DR HSP; P25445; IDDF.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004888; F:transmembrane receptor activity; IEA.
DR GO; GO:0006915; P:apoptosis; IEA.
DR GO; GO:0006955; P:immune response; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH_like.
DR InterPro; IPR008063; Fas_receptor.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 2.
DR PRINTS; PR01680; FASRECEPTOR.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
SQ SEQUENCE 327 AA; 36928 MW; 5CFEB844B2BB387A CRC64;

Query Match      22.4%; Score 243.5; DB 2; Length 327;
Best Local Similarity 31.2%; Pred. No. 7e-13;
Matches 48; Conservative 36; Mismatches 63; Indels 7; Gaps 5;

QY 48 CPAGEYWSKDVCCCKNSAGTFVKAPCEIPHTQGQCEKCHPG-TFTEKONYLDACILCSTC 106
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Db 47 CQSGLYNEHLFCCQPCPPGKRGKNGDKCRGDGMPCEVLCSEGNETDSSHSDKIRCVC 106
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QY 107 DKDQ--EMVADCSATSDRKCCRTGLYYDYKPEBSCBCTCKCQGIPLVLOECNSTANTV 164
Db 107 DEEHGLEVEHNCRTQNTQCKCKGN-PFCNSSPCEHCNPCTTCEHGI--IEKPTPTSNTK 163

QY 165 CSSSVSNPRNRLFLLLSLPLSLVSVVVFRIIR 198
Db 164 CKGSRSH-TNSIALLILLILLILFLIYKVVR 196

RESULT 13
Q678B7 PRELIMINARY; PRT; 289 AA.
AC Q678B7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Hypothetical protein.
OS Lymphocystis disease virus - isolate China.
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.
OX NCBI_TaxID=256729;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;
RZ Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;
RT "Complete Genome Sequence of Lymphocystis Disease Virus Isolated from
RT China.";
RL J. Virol. 78:6982-6994 (2004).
DR EMBL; AY380826; AAU10940.1; -.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS01186; EGF_2; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Hypothetical protein.
SQ SEQUENCE 289 AA; 32691 MW; 2686114D5D6C3F CRC64;

Query Match 22.0%; Score 239.5; DB 2; Length 289;
Best Local Similarity 38.7%; Pred. No. 1.4e-12;
Matches 55; Conservative 13; Mismatches 49; Indels 25; Gaps 5;

QY 24 LLLLLLLNLPLOVKFAMLELHSPKAGEYWSKDVCKNCNSAGTFVKAPCEIPHQTQCE 83
Db 1 MMLFILFLPITVHTAT-----DCPPGYIISKVY-----PAGT-----PMCS 37

QY 84 KCHFGTETKDNVLDACILCSTCDKQDEMVAADCSATSDRKCCRTGLYYDPKFPESCRP 143
Db 38 PCSFGTYTGLQSLRKLRCSTCSHNEPKVACSTTSDVQCQCRQG-YYIDPE-SEMCFF 95

QY 144 CTKCPQGIPLVLOECNSTANTVC 165
Db 96 CSNCESSKVKVTTCNRTHDTVC 117

RESULT 14
Q95185 PRELIMINARY; PRT; 189 AA.
AC Q95185;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumour necrosis factor receptor p60 (Fragment).
GN Name=TNFR-1;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RZ Duchie S., Nasir L., Eckersall P.D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.

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DR HSSP; P19438; IEXT.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000345; Cyt_c_heme_BS.
DR InterPro; IPR006209; EGF like.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor.
FT NON TER. 189
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CE809D7DBE CRC64;

Query Match 22.0%; Score 239; DB 2; Length 189;
Best Local Similarity 35.3%; Pred. No. 1e-12;
Matches 55; Conservative 19; Mismatches 70; Indels 12; Gaps 5;

QY 22 LLLLLLLNLPLOVKFAM-----LELHSPKAGEY---WSKDVCKNCNSAGTFVKAPC 73
Db 13 LVLLALLVEIYPLRVTLGLVPHLRDRKRAIPLCPQGYIHPQDINSICCTCKHGTYLYNDC 72

QY 74 EIPHTQCEKCHPGTETKDNVLDACILCSTCDKQ--QEMVADCSATSDRKCCRTGLY 131
Db 73 EGPGLDTDCRENGTFTASENYLRQCLSKCKRKMVQVEISPCTVYRDTVCGRKNQY 132

QY 132 -YYDPKFPESCRPCTCKPQGIPLVLOECNSTANTVCS 166
Db 133 RYWSETHFQCLNCSCLNG-TVQISCKETQNTVCT 167

RESULT 15
TNR6_BOVIN STANDARD; PRT; 323 AA.
AC P51857;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tumour necrosis factor receptor superfamily member 6 precursor (FASL
DE receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen)
DE (CD95 antigen)
GN Name=TNFRSF6; Synonyms=APT1, FAS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96226401; PubMed=8634151;
RA Yoo J., Stone R.T., Beattie C.W.;
RT "Cloning and characterization of the bovine Fas.";
RL DNA Cell Biol. 15:227-234 (1996).
CC -1- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD
CC recruits caspase-8 to the activated receptor. The resulting death-
CC inducing signaling complex (DISC) performs caspase-8 proteolytic
CC activation which initiates the subsequent cascade of caspases
CC (aspartate-specific cysteine proteases) mediating apoptosis. FAS-
CC mediated apoptosis may have a role in the induction of peripheral
CC tolerance, in the antigen-stimulated suicide of mature T-cells, or
CC both (By similarity).
CC -1- SUBUNIT: Binds DAXX and RIPK1 (By similarity).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: Contains a death domain involved in the binding of FADD,
CC and maybe to other cytosolic adaptor proteins.
CC -1- SIMILARITY: Contains 1 death domain.
CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 12:38:16 ; Search time 7215.45 Seconds  
(without alignments)  
4714.267 Million cell updates/sec

Title: US-10-622-407-9

Perfect score: 702

Sequence: 1 ttgcaatcgccatgttgg.....ttttattgctgaagtat 702

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.\*

1: gb\_ba.\*

2: gb\_hgt.\*

3: gb\_in.\*

4: gb\_om.\*

5: gb\_ov.\*

6: gb\_pat.\*

7: gb\_ph.\*

8: gb\_pl.\*

9: gb\_pr.\*

10: gb\_ro.\*

11: gb\_sts.\*

12: gb\_sy.\*

13: gb\_un.\*

14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	602	85.8	691	10 AY165627	AY165627 Mus muscu
4	602	85.8	1550	6 AR403753	AR403753 Sequence
5	594.4	84.7	1555	10 AY046551	AY046551 Mus muscu
6	578.6	82.4	669	10 MMU278265	AJ278265 Mus muscu
7	511	72.8	1200	6 AR403757	AR403757 Sequence
8	412	58.7	412	6 AR403752	AR403752 Sequence
9	377.4	53.8	531	10 AY046550	AY046550 Mus muscu
10	377.4	53.8	569	10 MMU278264	AJ278264 Mus muscu
11	377.4	53.8	1491	10 AY165625	AY165625 Mus muscu
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13	136.6	19.5	203141	10 AC068006	AC068006 Mus muscu
14	136.6	19.5	281000	10 MMU276505	AJ276505 Mus muscu
15	131.2	18.7	262	6 C0731135	C0731135 Sequence
16	115	16.4	272	6 C0742972	C0742972 Sequence
17	92.8	13.2	240262	2 AC129151	AC129151 Rattus no
18	87	12.4	2730	5 AB080946	AB080946 Parali
19	80.4	11.5	615	6 AX467100	AX467100 Sequence

20	80.4	11.5	2977	10 AY165628	AY165628 Mus muscu
21	73.2	10.4	615	6 AX467107	AX467107 Sequence
22	71	10.1	855	5 AY251409	AY251409 Gallus ga
23	71	10.1	1290	5 AY251408	AY251408 Gallus ga
24	69.8	9.9	1711	5 AF250042	AF250042 Danio rer
25	69.4	9.9	866	5 CR352587	CR352587 Gallus ga
26	60.2	8.6	65	6 CQ558638	CQ558638 Sequence
27	56.2	8.0	1187	5 BC074299	BC074299 Xenopus l
28	56.2	8.0	1239	5 AB111446	AB111446 Xenopus l
29	55.4	7.9	1451	5 AF302789	AF302789 Danio rer
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33	52.8	7.5	1161	5 CR761221	CR761221 Xenopus t
34	52.8	7.5	1223	5 BC075302	BC075302 Xenopus t
35	52.4	7.5	216329	2 AC123379	AC123379 Rattus no
36	51.6	7.4	258847	2 AC112746	AC112746 Rattus no
37	51.4	7.3	151652	2 AC128137	AC128137 Rattus no
38	51.2	7.3	222541	2 AC131076	AC131076 Mus muscu
39	50.6	7.2	199001	2 AC136115	AC136115 Rattus no
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41	50.4	7.2	206248	10 AC132453	AC132453 Mus muscu
42	50.4	7.2	221544	2 AC127862	AC127862 Rattus no
43	50.4	7.2	229910	2 AC135698	AC135698 Rattus no
44	50.4	7.2	239553	2 AC123201	AC123201 Rattus no
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## ALIGNMENTS

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VERSION	GI:40151462				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 702)				
AUTHORS	Saris, C.				
TITLE	Isolation, identification and characterization of tmst2, a novel member of the TNF-receptor supergene family				
JOURNAL	Patent: US 6627199-A 9 30-SEP-2003;				
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Db	1	TTGCACCTCGGCCATGTTGGCTTCTTCTGCAGCTTGGTGTCCAGTCTGAGTGGCTGTC	60		
Qy	61	CTTTGGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	120		
Db	61	CTTTGGCGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	120		
Qy	121	AAATTGCTATGTAGTAATTTACACTCTTCAATGTCCTGCTGCTGCTGCTGCTGCTGCTG	180		
Db	121	AAATTGCTATGTAGTAATTTACACTCTTCAATGTCCTGCTGCTGCTGCTGCTGCTGCTG	180		
Qy	181	GACCTGCTGTTGCAAGAACTGTTCTGCAAGTACATTTTGTCAAGGCGCCCTCGAAATCCCC	240		
Db	181	GACCTGCTGTTGCAAGAACTGTTCTGCAAGTACATTTTGTCAAGGCGCCCTCGAAATCCCC	240		
Qy	241	CATACCTCAAGGACAAATGTGAGAAAGTGTGACCCAGGAACATTTCACAGAGAAAGATAATTAC	300		

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Qy 541 GCCTGGCCTATCTGAATGGTTCACAGAGATCCAGAAACCGGCTGTTCCTACTGTTATCA 600
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RESULT 2  
AY165626  
LOCUS  
DEFINITION Mus musculus decoy TRAIL receptor 2 short form (Dctrailr2) mRNA,  
complete cds; alternatively spliced.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
AY165626.1 GI:27985789

ORGANISM  
Mus musculus (house mouse)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 736)  
Schneider,P., Olson,D., Tardivel,A., Browning,B., Lugovskoy,A.,  
Gong,D., Dobles,M., Hertig,S., Hofmann,K., Van Vlijmen,H.,  
Heu,Y.-M., Burkly,L., Tschopp,J. and Zheng,T.S.  
Identification of a New Murine Tumor Necrosis Factor Receptor Locus  
That Contains Two Novel Murine Receptors for Tumor Necrosis  
Factor-related Apoptosis-inducing Ligand (TRAIL)  
J. Biol. Chem. 278 (7), 5444-5454 (2003)  
12466268

JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
2 (bases 1 to 736)  
Schneider,P., Olson,D., Tardivel,A., Browning,B., Lugovskoy,A.,  
Gong,D., Dobles,M., Hertig,S., Hofmann,K., Van Vlijmen,H.,  
Heu,Y.-M., Burkly,L., Tschopp,J. and Zheng,T.S.  
Direct Submission  
Submitted (16-OCT-2002) Institute of Biochemistry, University of  
Lausanne, Boveresses 155, Epalinges CH-1066, Switzerland  
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1. .736  
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/strain="NIH Swiss"  
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31. .573  
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alternatively spliced  
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ANTVCSSSVRSRSASVAWPI"

## ORIGIN

Query Match 100.0%; Score 702; DB 10; Length 736;  
Best Local Similarity 100.0%; Pred. No. 8e-182;  
Matches 702; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 TTGCACCTCGGCCCATGTTTGGCTTCTTCTGCAGCTTGGTCCAGTCTGAGTCTGCTGTTT 60  
Db 19 TTGCACCTCGGCCCATGTTTGGCTTCTTCTGCAGCTTGGTCCAGTCTGAGTCTGCTGTTT 78  
Qy 61 CTTTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120  
Db 79 CTTTGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 138  
Qy 121 AAATTTGCTATGCTAGAAATTTACACTCCTTCAAAATGTCCTGCTGCTGCTGCTGCTGCTG 180  
Db 139 AAATTTGCTATGCTAGAAATTTACACTCCTTCAAAATGTCCTGCTGCTGCTGCTGCTGCT 198  
Qy 181 GAGCTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCGAAGCGCCCTCGAAATCCCC 240  
Db 199 GAGCTCTGTTGCAAGAACTGTTCTGCAGGTACATTTGTCGAAGCGCCCTCGAAATCCCC 258  
Qy 241 CATACTCAAGGACAAATGTGAGAAAGTGCACCCAGGAAACATTTCACAGAGAAAGATAATTAC 300  
Db 259 CATACTCAAGGACAAATGTGAGAAAGTGCACCCAGGAAACATTTCACAGAGAAAGATAATTAC 318  
Qy 301 CTGGATGCTTGTATATTTTGTCTCCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGC 360  
Db 319 CTGGATGCTTGTATATTTTGTCTCCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGC 378  
Qy 361 TCAGCCACAGTACCGGAAATGCCAGTGGCCGAGCAGTCTTTACTACTATGACCCAAA 420  
Db 379 TCAGCCACAGTACCGGAAATGCCAGTGGCCGAGCAGTCTTTACTACTATGACCCAAA 438  
Qy 421 TTTCCAGAAATCGTGGCGCCCAATGTACCAAGTGTCCCAAGGAAATCCCTGTCTCCAGGAA 480  
Db 439 TTTCCAGAAATCGTGGCGCCCAATGTACCAAGTGTCCCAAGGAAATCCCTGTCTCCAGGAA 498  
Qy 481 TGCAACTCCACAGCTAACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 540  
Db 499 TGCAACTCCACAGCTAACACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 558  
Qy 541 GCCTGGCCTATCTGAATGGTTCACAGAGATCCAGAAACCGGCTGTTCCTACTGTTATCA 600  
Db 559 GCCTGGCCTATCTGAATGGTTCACAGAGATCCAGAAACCGGCTGTTCCTACTGTTATCA 618  
Qy 601 CTTTGGATGCTGCTAAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660  
Db 619 CTTTGGATGCTGCTAAATGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 678  
Qy 661 TACAGATGTTTCTTAGCTTCTCTTTTATTTGCTATGAAGTGAT 702  
Db 679 TACAGATGTTTCTTAGCTTCTCTTTTATTTGCTATGAAGTGAT 720

RESULT 3  
AY165627  
LOCUS  
DEFINITION Mus musculus decoy TRAIL receptor 2 long form (Dctrailr2) mRNA,  
complete cds; alternatively spliced.  
ACCESSION  
VERSION  
KEYWORDS  
AY165627.1 GI:27986023

[illegible]





	/sub_species="domesticus" /db_xref="taxon:10092" /chromosome="7" 1. .669 /gene="Tnfrh2" 83..508 /gene="Tnfrh2" /codon_start=1 /evidence=experimental /product="tumor necrosis factor receptor p60 homologue 2" /protein_id="CAC16406.1" /db_xref="GI:11191812" /db_xref="GOA:Q9ER62" /db_xref="UniProt/Swiss-Prot:Q9ER62" /translation="MLELHSFKPAGEYMSKDVCCNKSAGTFVKAPEIPHTQGQCE KCHPGFTPKDNYLDACILCSTCKDQEMVADCSATSDRKCQCRCRTGLYYDPKFPSSC RPCTKCPQGIPLVLQECNSTANTVCSSSVSRSSASVAWPI"	
gene		
CDS		
	Query Match 82.4%; Score 578.6; DB 10; Length 669; Best Local Similarity 97.3%; Pred. No. 6.9e-148; Matches 640; Conservative 0; Mismatches 12; Indels 6; Gaps 5;	
QY	46 CTGAGTCGTGGTTCTTTGGCGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGAAT 105       	
Db	1 CTGAGTCGTGGTTCTTTGGCGCGGCTCTGCTG--TGCTGNTGNTG-- -TTGTTAAAT 57 	
QY	106 CTCGCCCTTGACAGGTAAAATT--GCTATGCTAGAATAACACTCTCTCAAAATGTCGCCGTGG 164 	
Db	58 CTCGCCCTTGACAGTAATAATTGGCATGCTAGAATAACACTCTCTCAAAATGTCGCCGTGG 117 	
QY	165 TGAATACTGCTTAAAGACGCTCTGTTGCAGAGAACTGTTCTGCAGGTACATTTGTCAAGGC 224 	
Db	118 TGAATACTGCTTAAAGACGCTCTGTTGCAGAGAACTGTTCTGCAGGTACATTTGTCAAGGC 177 	
QY	225 GCCTCGGAAATCCCCATFACTCAAGACAATGTGAGAAGTGTACCAGGAAACATTCCAC 284 	
Db	178 GCCTCGGAAATCCCCATFACTCAAGACAATGTGAGAAGTGTACCAGGAAACATTCCAC 237 	
QY	285 AGAAGAAGATAATTACTCGATGCTTGTATCTTTGCTCCACCTGTGTATAAAGATCAGGA 344 	
Db	238 AGAAGAAGATAATTACTCGATGCTTGTATCTTTGCTCCACCTGTGTATAAAGATCAGGA 297 	
QY	345 AATGGTGGCCGACTGCTCAGCCACCACTGACCGGAAATGCCAGTGCCGAAACAGGTCTTTTA 404 	
Db	298 AATGGTGGCCGACTGCTCAGCCACCACTGACCGGAAATGCCAGTGCCGAAACAGGTCTTTTA 357 	
QY	405 CTAATATGACCCAAAAATTTCCAGAAATCGTGCGCGCCAATGTATCCAGTGTCCCAGGAAT 464 	
Db	358 CTAATATGACCCAAAAATTTCCAGAAATCGTGCGCGCCAATGTATCCAGTGTCCCAGGAAT 417 	
QY	465 CCCTGTCTCCAGGAATGCAACTCCAGACTAACACGTGTGCAGTTCATCTGTITCAAG 524 	
Db	418 CCCTGTCTCCAGGAATGCAACTCCAGACTAACACGTGTGCAGTTCATCTGTITCAAG 477 	
QY	525 AAGATCTGCCTCAGTGGCCTGGCCTATCTCGAATGGTTTCCAGAGATCCCAGAAACCGGCT 584 	
Db	478 AAGATCTGCCTCAGTGGCCTGGCCTATCTGNAATGGTTCCAGAGATCCCAGAAACCGGCT 537 	
QY	585 GTTCCTACTGTTATCACCTTTGAGTGTGCTAAATGTGTCCGTTGTGTCCTCCGTATCAT 644 	
Db	538 GGTCCTACTGTTATCACCTTTGAGTGTGCTAAATGTGTCCG--TGGTGGCCTCCGTATCAT 596 	
QY	645 AAGNAGATAAGGTTCTACAGATGTTTTCTTAGTCTCTTTTATTTGCTATGAGTGTAT 702 	
Db	597 AAGAAGATAAAGG--TCTACAGATGTTTTCTTANCTTCTCTTTTATTTGCTATGAGTGTAT 653 	
ORIGIN		
RESULT 7		
AR403757	LOCUS AR403757 1200 bp DNA linear PAT 18-DEC-2003	
DEFINITION	Sequence 13 from patent US 6627199.	
ACCESSION	AR403757	







Center: Whitehead Institute/MIT Center for Genome Research  
 Center code: WIBR  
 Web site: <http://www-seq.wi.mit.edu>  
 Contact: [sequence\\_submissions@broad.mit.edu](mailto:sequence_submissions@broad.mit.edu)  
 ----- Project Information -----  
 Center project name: L5724  
 Center clone name: 6\_I\_17  
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Some of the sequence contained within base pairs 1 - 31513 was  
 stolen from accession AC023248.

## FEATURES

## source

1. 203141  
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 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
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 /chromosome="7"  
 /map="7"  
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1. 6750  
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1543..1580  
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2281..2370  
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2340..2498  
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2517..2675  
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2824..2873  
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5411..5445  
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5614..5655  
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Query Match 19.5%; Score 136.6; DB 10; Length 203141;

Best Local Similarity 94.0%; Pred. No. 2.8e-26; Matches 142; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 198 CTGTTCTGCAGGTACATTTGTCAAGCGCCCTCGGAATCCCAATCCCAATCAAGGACAATG 257  
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 Db 149180 CTTATCCCAGGTACATTTGTCAAGCGCCCTCGGAATCCCAATCAAGGACAATG 149121  
 Qy 258 TGAGAAAGTGTACCCAGGAACATTCACAGAAAGATAATTAATCTGATGCTGTGTATCT 317  
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 Db 149120 TGAGAAAGTGTACCCAGGAACATTCACAGAAAGATAATTAATCTGATGCTGTGTATCT 149061  
 Qy 318 TTGCTCCACTGTGATATAAGATCAGGAATG 348  
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 Db 149060 TTGCTCCACTGTGATATAAGATGATGTG 149030

## RESULT 14

## MMU276505

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## TITLE

MMU276505 281000 bp DNA linear ROD 06-MAR-2002  
 Mus musculus genomic fragment, 281000 bp, chromosome 7.

AJ276505

AJ276505.2 GI:12583595

car3 gene; Cdkn1c gene; cyclin-dependent kinase inhibitor 1C;  
 cysteinyl-tRNA-synthetase; IPL gene; Itm gene; Nap114 gene;  
 nucleosome assembly protein 1-like 4 protein; Obp1 gene; oxysterol  
 binding protein; Tnfrh2 gene; Tnfrh2 gene; tumor necrosis factor  
 receptor p60 homologue 1; tumor necrosis factor receptor p60  
 homologue 2; tumor suppressing subtransferable candidate 5.

Mus musculus domesticus (western European house mouse)

Mus musculus domesticus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

## REFERENCE

## AUTHORS

## TITLE

## SEQUENCE AND FUNCTIONAL COMPARISON IN THE BECKWITH-WIEMANN

region: implications for a novel imprinting centre and extended  
imprinting  
Hum. Mol. Genet. 9 (18), 2691-2706 (2000)  
20519229  
11063728  
REFERENCE  
2  
AUTHORS  
Engemann.S.  
Direct Submission  
Submitted (17-MAR-2000) Engemann S., Dep. Trautner,  
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195  
Berlin, GERMANY  
Revised by author 22-MAY-2000  
3 (bases 1 to 281000)  
Engemann.S.  
Direct Submission  
Submitted (22-NOV-2000) Engemann S., Dep. Trautner,  
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195  
Berlin, GERMANY  
4 (bases 1 to 281000)  
Engemann.S.  
Direct Submission  
Submitted (24-JAN-2001) Engemann S., Dep. Trautner,  
Max-Planck-Institut fuer Molekulare Genetik, Ihnestrasse 73, 14195  
Berlin, GERMANY  
COMMENT  
On Jan 27, 2001 this sequence version replaced gi:1191799.  
related accession numbers AJ300452-AJ300460  
has a 1000 bp overlap with AJ271885.  
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13783..13967,14347..14428,15828..15926,16308..16404,  
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27169..27307)  
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SVWAVKPGESVSTIOTPLPSSYLI1FRAASESDGRCWLDALALRCSSLLRLSTCK  
QGRDEQSSPDSPSSLYGLPTSATIPDQDLFPLNGSALENDAFSDKSERENAEEDSD  
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/db\_xref="GOA:Q9ER63"  
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Query Match 19.5%; Score 136.6; DB 10; Length 281000;  
Best Local Similarity 94.0%; Pred. No. 2.8e-26;  
Matches 142; Conservative 0; Mismatches 9; Indels 0; Gaps 0;  
Qy 198 GTGTTCTGCGAGTACATTTGTCAAGGGCCCTGCGAAATCCCCATACCTCAAGGACAATG 257  
Db 73700 CTTATCCCGAGTACATTTGTCAAGGGCCCTGCGAAATCCCCATACCTCAAGGACAATG 73759  
Qy 258 TGAGAAGTGTCAAGGACAATTTCAAGGACAATTTACCTGGATGCTGTGTACT 317  
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Qy 318 TTGCTCCACCTGTGATAAAGATCAGGAAATG 348  
Db 73820 TTGCTCCACCTGTGATAAAGTGTGTGTG 73850

RESULT 15  
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LOCUS CQ731135 262 bp DNA linear PAT 03-FEB-2004  
DEFINITION Sequence 17069 from Patent WO02068579.  
ACCESSION CQ731135  
VERSION CQ731135.1 GI:42306906  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1  
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.  
TITLE Kits, such as nucleic acid arrays, comprising a majority of  
humanexons or transcripts, for detecting expression and other uses  
thereof  
JOURNAL Patent: WO 02068579-A 17069 06-SEP-2002;  
PE Corporation (NY) (US)  
FEATURES Location/Qualifiers

source 1..262  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"  
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Best Local Similarity 75.2%; Pred. No. 7.4e-25;  
Matches 197; Conservative 0; Mismatches 23; Indels 42; Gaps 1;  
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Qy 178 AAAGACGTCTGTTGCAAGAACTGTTCTGCA----- 207  
Db 61 AATGATGTCTGTTGCAAGACCTGTCCTCAGGTGAGTTCTTCAATGAGACCCAGTGCCAC 120  
Qy 208 -----GGTACATTTGTCAAGGGCCCTGCGAAATCCCCATACCTCAAGGACA 255  
Db 121 AGCATAGACATGGGTACATTTGTCAAGGGCCCTGCGAAATCCCCATACCTCAAGGACA 180  
Qy 256 TGTGAGAAGTGTCAAGGACAATTTCAAGGACAATTTACCTGGATGCTGTGTATA 315  
Db 181 TGTGAGAAGTGTCAAGGACAATTTCAAGGACAATTTACCTGGATGCTGTGTATA 240  
Qy 316 CTTTGTCTCCACCTGTGTATAAAG 337  
Db 241 CTTTGTCTCCACCTGTGTATAAAG 262

Search completed: September 8, 2005, 23:31:27  
Job time : 7219.45 secs



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Qy 441 P-

QY  
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Best Local Similarity	90.7%;	Pred.	No. 2e-110;					
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Qy	141	ACACTCTCTCAAAATGTCCTCCGCTGGTGAATACTTGGTCTAAAAGACGCTGTTGTGCAAGAACTG	200					
Dd	110	ATACTCTTCAAATGTCCTCCGATGGTGAATACCAGTCTAATGATGCTGTTGTCAGAACCTG	169					
Qy	201	TTCCTGCAAGTGACAATTTGTCGAAGCGCCCTGCGAAATCCCCCATACTCAAGGACAATGTGA	260					
Dd	170	TCCCTCAGGTAGACATTTGTCGAAGCGCCCTGCAAAATCCCCCATACTCAAGGACAATGTGA	229					
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Dd	230	GAAGTGTCACCGAGAACATTTCACAGGGAAGATAATGGCGTGCATGATTGTGTGAACCTTTG	289					
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APPLICATION NUMBER: US 60/045,233  
FILING DATE: 17-APR-1997  
APPLICATION NUMBER: WO PCT/US97/16033  
FILING DATE: 10-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 014210-000730US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2224 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
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NAME/KEY: -  
LOCATION: 1..2224  
OTHER INFORMATION: /note= "rat small conductance,  
calcium-activated potassium channel  
protein 3 (rsk3) full-length cDNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 44:

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Best Local Similarity 62.7%; Pred. No. 0.0002;  
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
Qy 2 TGCACCTGGCCAGTGTGGCTTCTTCGACAGTGTGTCAGTCTGAGTGGTTC 61  
Db 309 TGCAACAGACAGATGACAACTGGCTCTGGAGTTGGGCAAGCTGAGGCGGGTGC 250  
Qy 62 TTTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119  
Db 249 AGTGGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192

## RESULT 13

US-10-116-260-44/c  
Sequence 44, Application US/10116260  
Patent No. 6828123  
GENERAL INFORMATION:  
APPLICANT: Adelman, John P.  
Maylie, James  
Bond, Chris T.  
Silvia, Christopher P.  
TITLE OF INVENTION: Small and Intermediate Conductance,  
Calcium-Activated Potassium Channels and Uses  
Thereof  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/116,260  
FILING DATE: 03-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/254,590  
FILING DATE: 10-Mar-1999  
APPLICATION NUMBER: US 60/026,451

FILING DATE: 11-SEP-1996  
APPLICATION NUMBER: US 60/040,052  
FILING DATE: 07-MAR-1997  
APPLICATION NUMBER: US 60/045,233  
FILING DATE: 17-APR-1997  
APPLICATION NUMBER: WO PCT/US97/16033  
FILING DATE: 10-SEP-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 014210-000730US  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2224 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: -  
LOCATION: 1..2224  
OTHER INFORMATION: /note= "rat small conductance,  
calcium-activated potassium channel  
protein 3 (rsk3) full-length cDNA"  
SEQUENCE DESCRIPTION: SEQ ID NO: 44:

Query Match 6.8%; Score 47.6; DB 4; Length 2224;  
Best Local Similarity 62.7%; Pred. No. 0.0002;  
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;  
Qy 2 TGCACCTGGCCAGTGTGGCTTCTTCGACAGTGTGTCAGTCTGAGTGGTTC 61  
Db 309 TGCAACAGACAGATGACAACTGGCTCTGGAGTTGGGCAAGCTGAGGCGGGTGC 250  
Qy 62 TTTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119  
Db 249 AGTGGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192

## RESULT 14

US-10-115-671-44/c  
Sequence 44, Application US/10115671  
Patent No. 6828420  
GENERAL INFORMATION:  
APPLICANT: Adelman, John P.  
Maylie, James  
Bond, Chris T.  
Silvia, Christopher P.  
TITLE OF INVENTION: Small and Intermediate Conductance,  
Calcium-Activated Potassium Channels and Uses  
Thereof  
NUMBER OF SEQUENCES: 48  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/115,671  
FILING DATE: 03-Apr-2002  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:

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; APPLICATION NUMBER: US/09/254,590
; FILING DATE: 10-Mar-1999
; APPLICATION NUMBER: US 60/026,451
; FILING DATE: 11-SEP-1996
; APPLICATION NUMBER: US 60/040,052
; FILING DATE: 07-MAR-1997
; APPLICATION NUMBER: US 60/045,233
; FILING DATE: 17-APR-1997
; APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 014210-000730US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2224 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2224
; OTHER INFORMATION: /note= "rat small conductance,
; calcium-activated potassium channel
; protein 3 (rsk3) full-length cDNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 44:
US-10-115-671-44

Query Match 6.8%; Score 47.6; DB 4; Length 2224;
Best Local Similarity 62.7%; Pred. No. 0.0002;
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 2 TGCACCTGGCCATGTTGGCTTCTTCGACGCTGGTGTCAGCTGAGTCGCTGGTTC 61
Db |||||
309 TGCACACAGCAGGATGACAACTGGCTCTGGAGTTGGGCAAGCTGAGGCGGGGTGC 250
Qy 62 TTTCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119
Db |||||
249 AGTGAGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 192

RESULT 15
US-09-922-364A-48/c
; Sequence 48, Application US/09922364A
; Patent No. 6692937
; GENERAL INFORMATION:
; APPLICANT: Adelman, John P.
; Maylie, James
; Bond, Chris T.
; Silvia, Christopher P.
; TITLE OF INVENTION: Small and Intermediate Conductance,
; Calcium-Activated Potassium Channels and Uses
; Thereof
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/922,364A
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; FILING DATE: 03-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/254,590
; FILING DATE: 10-Mar-1999
; APPLICATION NUMBER: US 60/026,451
; FILING DATE: 11-SEP-1996
; APPLICATION NUMBER: US 60/040,052
; FILING DATE: 07-MAR-1997
; APPLICATION NUMBER: US 60/045,233
; FILING DATE: 17-APR-1997
; APPLICATION NUMBER: WO PCT/US97/16033
; FILING DATE: 10-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 014210-000730US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 48:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2462 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: -
; LOCATION: 1..2462
; OTHER INFORMATION: /note= "human small conductance,
; calcium-activated potassium channel
; protein 3 (hsk3) full length cDNA"
; SEQUENCE DESCRIPTION: SEQ ID NO: 48:
US-09-922-364A-48

Query Match 6.8%; Score 47.6; DB 4; Length 2462;
Best Local Similarity 62.7%; Pred. No. 0.00021;
Matches 74; Conservative 0; Mismatches 44; Indels 0; Gaps 0;

Qy 2 TGCACTCGGCCATGTTGGCTTCTTCGACGCTGGTGTCAGTCTGAGTCGCTGGTTC 61
Db |||||
571 TGACAGCAGGCAGGTCGACGGGCTGGCTCTGGAGTTGGGGGAGCTGACAGCGGATGC 512
Qy 62 TTTGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119
Db |||||
511 GGTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 454

Search completed: September 9, 2005, 07:09:10
Job time : 353.87 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 12:35:36 ; Search time 1032.11 Seconds  
(without alignments)  
4026.354 Million cell updates/sec

Title: US-10-622-407-9

Perfect score: 702

Sequence: 1 ttgcaatcgccatgtttgg.....ttttattgtatgaagtat 702

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : N\_Geneseq\_16Dec04:\*

- 1: Geneseqn1980s:\*
- 2: Geneseqn1990s:\*
- 3: Geneseqn2000s:\*
- 4: Geneseqn2001as:\*
- 5: Geneseqn2001bs:\*
- 6: Geneseqn2002as:\*
- 7: Geneseqn2002bs:\*
- 8: Geneseqn2003as:\*
- 9: Geneseqn2003bs:\*
- 10: Geneseqn2003cs:\*
- 11: Geneseqn2003ds:\*
- 12: Geneseqn2004as:\*
- 13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	702	100.0	702	10	AAD64755 Mouse tms
2	702	100.0	702	12	Adj45753 Murine tm
3	602	85.8	1550	10	AAD64754 Mouse tms
4	602	85.8	1550	12	Adj45751 Murine tm
5	511	72.8	1200	10	AAD64758 Mouse tms
6	511	72.8	1200	12	Adj45757 Murine tm
7	412	58.7	412	10	AAD64753 Mouse tms
8	412	58.7	412	12	Adj45749 Murine tm
9	392.4	55.9	415	6	ABs69674 Novel mur
10	377.4	53.8	967	12	Adf57550 Mouse ymk
11	377.4	53.8	1509	2	AAV68046 Nucleic a
12	377.4	53.8	1509	12	Adm46622 Mouse 7P4
13	375.8	53.5	603	10	AdD33513 Mouse mit
14	253.2	36.1	357	12	Adf57563 Mouse ymk
15	221.8	31.6	1197	5	AA573531 DNA encod
16	80.4	11.5	615	6	ABN89334 Murine TA
17	60.2	8.6	65	6	ABN55525 Mouse spl
18	48.6	6.9	403	3	ABK10240 Trinucleo
19	48.4	6.9	4248	11	ACN90396 Breast ca
20	47.6	6.8	389	3	ABK10248 Tri-nucle

C	21	47.6	6.8	1269	10	ACC68996	ACC68996 Human neu
C	22	47.6	6.8	1379	5	AAS87787	AAS87787 DNA encod
C	23	47.6	6.8	1423	10	ACC68997	ACC68997 Human neu
C	24	47.6	6.8	1776	2	AA223425	AA223425 Human Mac
C	25	47.6	6.8	2224	2	AAV35472	AAV35472 Rat rSK3
C	26	47.6	6.8	2462	2	AAV35473	AAV35473 Human hSK
C	27	47.6	6.8	3095	9	ACF03947	ACF03947 Human SK-
C	28	47.6	6.8	3095	10	ABE311740	ABE311740 Human 122
C	29	47.2	6.7	1016	5	AAS79773	AAS79773 DNA encod
C	30	47	6.7	277	3	ABK10239	ABK10239 Trinucleo
C	31	46.8	6.7	504	4	ABL41663	ABL41663 Nucleotid
C	32	46.6	6.6	365	10	ACD94759	ACD94759 Human col
C	33	46.4	6.6	1080	4	ABL22295	ABL22295 Drosophil
C	34	46.4	6.6	5264	4	ABU22294	ABU22294 Drosophil
C	35	46.4	6.6	5824	4	ABL15249	ABL15249 Drosophil
C	36	46.4	6.6	11743	4	ABL15248	ABL15248 Drosophil
C	37	46.4	6.6	89873	13	ABD32846	ABD32846 Mouse can
C	38	46.2	6.6	1810	4	AAF84342	AAF84342 Human and
C	39	46.2	6.6	4719	12	ADJ92835	ADJ92835 Human co-
C	40	46.2	6.6	5257	6	ABV94246	ABV94246 Breast ca
C	41	46.2	6.6	5257	10	ADF56532	ADF56532 Fusion pr
C	42	46.2	6.6	5257	10	ADK67041	ADK67041 Gene #131
C	43	46.2	6.6	5830	12	ADP22722	ADP22722 Human SMA
C	44	46.2	6.6	5959	6	ABL66686	ABL66686 Lung canc
C	45	46.2	6.6	5959	6	ABK84651	ABK84651 Human CDN

#### ALIGNMENTS

##### RESULT 1

AAD64755

ID AAD64755 standard; cDNA; 702 BP.

XX AAD64755;

XX 11-MAR-2004 (first entry)

XX Mouse tmst2-receptor splice variant cDNA.

DE Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;

XX cachexia; autoimmune disease; inflammatory disease; chromosome mapping;

KW cancer; chromosome identification; gene therapy; antibacterial; virucide;

KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;

KW cytostatic; mouse; splice variant; gene; ss.

XX Mus musculus.

OS Mus musculus.

XX Key Location/Qualifiers

PH CDS 13..555

FT /\*tag= a

FT /product= "Mouse tmst2 receptor splice variant protein"

XX US6627199-B1.

PN 30-SEP-2003.

PD 07-JUL-2000; 2000US-00612033.

PF 09-JUL-1999; 99US-0143063P.

XX (AMGE-) AMGEN INC.

PA Saris C;

XX WPI; 2003-874309/81.

XX P-PSDB; ABW02716.

DR New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,

XX treating or ameliorating diseases associated with or resulting from

PT abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for

PT chromosome mapping.

XX

















Db 470 TGTGTGCAGTTCATCTGTTTCAA 492

RESULT 12

AD46622

ID ADM46622 standard; DNA; 1509 BP.

XX

AC ADM46622;

XX

DT 17-JUN-2004 (first entry)

XX

DE Mouse 7F4 encoding sequence.

XX

XX 7F4 gene; Osteopathic; Anorectic; Antidiabetic; glycolipid metabolism disorder; osteoporosis; obesity; diabetes; ds.

XX

OS Mus musculus.

XX

XX Key Location/Qualifiers

FT CDS 12..542

FT /\*tag= a

FT /\*tag= b

FT mat\_peptide 96..539

FT /\*tag= c

XX

PN WO9843998-A1.

XX

PD 08-OCT-1998.

XX

PP 01-APR-1998; 98WO-JP001511.

XX

PR 01-APR-1997; 97JP-00099653.

XX

PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX

PI Kimura N, Toyoshima T;

XX

DR WPI; 1998-568275/48.

DR P-PSDB; AAW80254.

XX

XX Receptor protein inducing differentiation in osteoblast cells - has extracellular region only and can be used for screening substances for treatment of bone growth disorders.

PT

PT Claim 2; Page 29-31; 51pp; Japanese.

XX

XX The present sequence encodes a protein designated 7F4. This protein is capable of inducing differentiation in osteoblast cells. The protein may be used to screen compounds for the ability to bind to it, for use as ligands, agonists or antagonists and inhibiting or otherwise altering its differentiation inducing activity. Compounds so identified, as well as the protein itself, DNA encoding it, and antibodies to it, may be used in the treatment of diseases of bone growth and osteoblast differentiation, such as bone sarcomas

XX

XX Sequence 1509 BP; 387 A; 403 C; 294 G; 425 T; 0 U; 0 Other;

Query Match 53.8%; Score 377.4; DB 2; Length 1509;

Best Local Similarity 90.7%; Pred. No. 3.4e-98;

Matches 402; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 81 GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCCAGGTAAATTTGCTATGCTAGAAAT 140

Db 50 GTTCCTTTGCTGCTGCTGCTGAATCTGTTCTTCCGGTAAATTTGCTATGCTAGATC 109

Qy 141 ACACTCTTCAAAATGTCGGCTGGTGAATACCTGGTCTAAAGACGTCCTGTTGCAAGACTG 200

Db 110 ATACTCTTCAACTGTCCGCTGGTGAATACCAAGTCTAATGATGCTCTGTTGCAAGACTG 169

Qy 201 TTCTGCGGTGACATTTGTCAAGCGCCCTGCGAATATCCCATCTCAAGGACATGTGA 260

Db 170 TCCTCAGGTACATTTGTCAAGCGCCCTGCGAATATCCCATCTCAAGGACATGTGA 229

Qy 261 GAAGTGTCAACAGGACATTTACAGAGAAAGATTAATACCTGGATGCTTGTATCTTTG 320

Db 230 GAAGTGTCAACAGGACATTTACAGAGAAAGATTAATGCTGATGTTGATGCTTTG 289

Qy 321 CTCACCTGTGATAAAGATCAGAAATGTTGGCCGACTGCTCAGGCAACAGTACCGGAA 380

Db 290 CTCACCTGTGATAAAGACAGAAATGTTGGCTGACTGTTCTGCGCACAGTACCGGAA 349

Qy 381 ATGCCAGTCCGACAGGCTTTTACTACTATGACCCAAATTTCCAGATCTGTCGCCGC 440

Db 350 ATGCCAGTCCGACAGGCTTTTACTACTATGACCCAAATTTCCAGATCTGTCGCCGC 409

Qy 441 ATGTACCAAGTGTCCCAAGGAATCCCTGCTCTCCAGGAATGCAACTCCACAGCTAACAC 500

Db 410 ATGTACCAAGTGTCCCAAGGAATCCCTGCTCTCCAGGAATGCAACTCCACAGCTAACAC 469

Qy 501 TGTGTGCGTTCATCTGTTTCAA 523

XX

XX Transgenic non-human animal with modified expression of 7F4 gene for screening remedies for bone or glycolipid metabolism disorders.

XX

XX Claim 3; SEQ ID NO 1; 44pp; Japanese.

XX

XX The present invention relates to a transgenic non-human animal having the expression of 7F4 gene artificially modified. The transgenic animals are a disease model for bone and glycolipid metabolism disorders. Substances identified by the screening method are agents for the prevention and treatment of diseases including osteoporosis, obesity and diabetes. The present sequence represents the modified mouse 7F4 encoding sequence.

XX

XX Sequence 1509 BP; 387 A; 403 C; 294 G; 425 T; 0 U; 0 Other;

Query Match 53.8%; Score 377.4; DB 12; Length 1509;

Best Local Similarity 90.7%; Pred. No. 3.4e-98;

Matches 402; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 81 GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCCAGGTAAATTTGCTATGCTAGAAAT 140

Db 50 GTTCCTTTGCTGCTGCTGCTGAATCTGTTCTTCCGGTAAATTTGCTATGCTAGATC 109

Qy 141 ACACTCTTCAAAATGTCGGCTGGTGAATACCTGGTCTAAAGACGTCCTGTTGCAAGACTG 200

Db 110 ATACTCTTCAACTGTCCGCTGGTGAATACCAAGTCTAATGATGCTCTGTTGCAAGACTG 169

Qy 201 TTCTGCGGTGACATTTGTCAAGCGCCCTGCGAATATCCCATCTCAAGGACATGTGA 260

Db 170 TCCTCAGGTACATTTGTCAAGCGCCCTGCGAATATCCCATCTCAAGGACATGTGA 229

Qy 261 GAAGTGTCAACAGGACATTTACAGAGAAAGATTAATACCTGGATGCTTGTATCTTTG 320

Db 230 GAAGTGTCAACAGGACATTTACAGAGAAAGATTAATGCTGATGTTGATGCTTTG 289

Qy 321 CTCACCTGTGATAAAGATCAGAAATGTTGGCCGACTGCTCAGGCAACAGTACCGGAA 380

Db 290 CTCACCTGTGATAAAGACAGAAATGTTGGCTGACTGTTCTGCGCACAGTACCGGAA 349

Qy 381 ATGCCAGTCCGACAGGCTTTTACTACTATGACCCAAATTTCCAGATCTGTCGCCGC 440

Db 350 ATGCCAGTCCGACAGGCTTTTACTACTATGACCCAAATTTCCAGATCTGTCGCCGC 409

Qy 441 ATGTACCAAGTGTCCCAAGGAATCCCTGCTCTCCAGGAATGCAACTCCACAGCTAACAC 500

Db 410 ATGTACCAAGTGTCCCAAGGAATCCCTGCTCTCCAGGAATGCAACTCCACAGCTAACAC 469

Qy 501 TGTGTGCGTTCATCTGTTTCAA 523

Db	290	CTCCACCTGTGATAAAGACCAGATATAGGTGGCTGACTGTTCTGCCACCAGTGACCGGAA	349
Qy	381	ATGCCAGTCCCGAAGAGCTTTTACTACTATGACCCAAAATTTCCAGAAATCGTGGCGCCC	440
Db	350	ATGCCAGTGCCAAATAGGCTTTTACTATGACCCAAAATTTCCGGAATCATGCGGCC	409
Qy	441	ATGTACCAAGTGTCCCCAAGNAATCCCTGTCTCGAGGATGCAATCTCCACAGCTAACAC	500
Db	410	ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCGAGGATGCAATCTCCACAGCTAACAC	469
Qy	501	TGTGTCAGTTTCATCTGTTTCAA	523
Db	470	TGTGTGCAGTTTCATCTGTTTCAA	492

## RESULT 13

ADD33513

ID ADD33513 standard; DNA; 603 BP.

XX

AC ADD33513;

XX  
DT 15-JAN-2004 (first entry)

Mouse mitochondrial DNA sequence SEO ID NO:1286.

ds; mouse; array; mitochondrial; hybridisation; energy-metabolism;  
KW  
KW  
mitochondrial disease; oxidative phosphorylation dysfunction;  
KW  
oxidative stress; apoptosis; aging.  
KW

OS Mus musculus.

XX  
PN  
WO2003020220-A2.

XX  
PD  
13-MAR-2003.

30-AUG-2002; 2002WO-US027886.

XX  
PR 30-AUG-2001; 2001US-0316323P.

PR 31-AUG-2001; 2001CA-02356540.

XX  
PA (UYEM-) UNIV EMORY.

PI Wallace DC, Levy S, Kerstann K, Procaccio V;  
XX

XX  
DR WPI: 2003-300821/29.

XX Array containing probes for genes involved in mitochondrial biology,  
PT useful for determining mitochondrial biology gene expression profiles for  
PT use in diagnosing pathologies and identifying biochemical pathways.

PS Claim 2: SEQ ID NO 1286: 201pp: English.

XX The invention relates to a novel array comprising at least two isolated  
CC nucleotide molecules, each molecule having a sequence capable of uniquely  
CC hybridising to a nucleic acid molecule which is an expression product of a  
CC gene involved in mitochondrial biology. The array comprises two or more  
CC isolated nucleic acid molecules or spots, each molecule having a sequence  
CC chosen from sequence of 994 human probes and 2046 mouse probes. An array  
CC of the invention is useful for determining an expression profile of a  
CC mouse or human sample containing nucleic acid, by contacting the array  
CC with the sample under conditions allowing selective hybridisation, and  
CC measuring hybridisation of nucleic acid in the sample to the array to  
CC produce an expression profile. The array is also useful for determining  
CC an expression profile of a first labelled sample containing nucleic acid  
CC relative to a second, differently labelled sample containing nucleic  
CC acid. The second sample is a reference or a standard. An array is useful  
CC for determining an expression profile diagnostic of an energy-metabolism-  
CC related physiological condition. An array of the invention is useful for  
CC determining mitochondrial biology gene expression profiles of organisms,  
CC such as human, mice and closely related species, tissue and organs of  
CC such organisms, which are useful for determining expression profiles  
CC diagnostic of energy metabolism-related physiological conditions.



Db 417 |||||CCCCATACCTCAAGGACAATGTGAGAGTGTACCCAGGAACATTCACAGAGAAAGATAA 476  
Qy 297 |||||TTACCTGGATGCTTGTATATACTTTGCTCCACCTGTGATATAAGATCA 341  
Db 477 |||||TTACCTGGATGCTTGTATATACTTTGCTCCACCTGTGATATAAGGTGA 521

Search completed: September 8, 2005, 17:05:23  
Job time : 1034.11 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 16:10:01 ; Search time 1594.46 Seconds  
(without alignments)  
2891.383 Million cell updates/sec

Title: US-10-622-407-9

Perfect score: 702

Sequence: 1 ttgcatcgccatgttggtttg.....ttttattgtatgaagtgat 702

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 7351250 seqs, 3283620254 residues

Total number of hits satisfying chosen parameters: 14702500

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Published Applications NA:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq.\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq.\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq.\*
- 5: /cgn2\_6/ptodata/1/pubpna/US07\_NEW\_PUB.seq.\*
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- 11: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq.\*
- 12: /cgn2\_6/ptodata/1/pubpna/US09\_NEW\_PUB.seq.\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10A\_PUBCOMB.seq.\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10B\_PUBCOMB.seq.\*
- 15: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq.\*
- 16: /cgn2\_6/ptodata/1/pubpna/US10D\_PUBCOMB.seq.\*
- 17: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq.\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10F\_PUBCOMB.seq.\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10G\_PUBCOMB.seq.\*
- 20: /cgn2\_6/ptodata/1/pubpna/US10H\_PUBCOMB.seq.\*
- 21: /cgn2\_6/ptodata/1/pubpna/US10I\_PUBCOMB.seq.\*
- 22: /cgn2\_6/ptodata/1/pubpna/US10J\_PUBCOMB.seq.\*
- 23: /cgn2\_6/ptodata/1/pubpna/US11A\_PUBCOMB.seq.\*
- 24: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq.\*
- 25: /cgn2\_6/ptodata/1/pubpna/US60\_NEW\_PUB.seq.\*
- 26: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Length	DB ID	Description
1	702	100.0	702	US-10-622-407-9 Sequence 9, Appli
2	602	85.8	17	US-10-622-407-7 Sequence 7, Appli
3	511	72.8	1200	US-10-622-407-13 Sequence 13, Appli
4	412	58.7	17	US-10-622-407-5 Sequence 5, Appli
5	392.4	55.9	415	US-09-728-445-737 Sequence 737, App
6	392.4	55.9	415	US-10-964-549-737 Sequence 737, Appl
7	377.4	53.8	967	US-10-193-616-7 Sequence 7, Appli

8	377.4	53.8	1509	9	US-09-855-266A-3	Sequence 3, Appli
9	377.4	53.8	1509	19	US-10-802-332-3	Sequence 3, Appli
10	253.2	36.1	357	14	US-10-193-616-5	Sequence 5, Appli
11	60.2	8.6	65	10	US-09-908-975-28273	Sequence 28273, A
12	48.4	6.9	4248	14	US-10-198-846-11546	Sequence 11546, A
13	47.6	6.8	1269	20	US-10-489-372-43	Sequence 43, Appli
14	47.6	6.8	1423	20	US-10-489-372-44	Sequence 44, Appli
15	47.6	6.8	2224	9	US-09-922-364A-44	Sequence 44, Appli
16	47.6	6.8	2224	9	US-09-254-590-44	Sequence 44, Appli
17	47.6	6.8	2224	13	US-10-115-695-44	Sequence 44, Appli
18	47.6	6.8	2224	14	US-10-116-561-44	Sequence 44, Appli
19	47.6	6.8	2224	14	US-10-115-671-44	Sequence 44, Appli
20	47.6	6.8	2224	14	US-10-115-415-44	Sequence 44, Appli
21	47.6	6.8	2224	14	US-10-116-260-44	Sequence 44, Appli
22	47.6	6.8	2224	15	US-10-115-688-44	Sequence 44, Appli
23	47.6	6.8	2393	21	US-10-278-698-70	Sequence 70, Appli
24	47.6	6.8	2393	21	US-10-278-698-584	Sequence 584, App
25	47.6	6.8	2462	9	US-09-922-364A-48	Sequence 48, Appli
26	47.6	6.8	2462	9	US-09-254-590-48	Sequence 48, Appli
27	47.6	6.8	2462	13	US-10-115-695-48	Sequence 48, Appli
28	47.6	6.8	2462	14	US-10-116-561-48	Sequence 48, Appli
29	47.6	6.8	2462	14	US-10-115-671-48	Sequence 48, Appli
30	47.6	6.8	2462	14	US-10-115-415-48	Sequence 48, Appli
31	47.6	6.8	2462	14	US-10-116-260-48	Sequence 48, Appli
32	47.6	6.8	2462	15	US-10-115-688-48	Sequence 48, Appli
33	47.6	6.8	3095	17	US-10-353-690-97	Sequence 97, Appli
34	46.4	6.6	89873	21	US-10-461-862-61	Sequence 61, Appli
35	46.2	6.6	4719	17	US-10-414-692-36	Sequence 36, Appli
36	46.2	6.6	5257	15	US-10-007-926A-237	Sequence 237, App
37	46.2	6.6	5257	21	US-10-956-157-995	Sequence 995, App
38	46.2	6.6	5864	21	US-10-956-157-4070	Sequence 4070, Ap
39	46.2	6.6	5959	9	US-09-954-456-1996	Sequence 1996, Ap
40	46.2	6.6	5959	21	US-10-843-641A-5023	Sequence 5023, Ap
41	46	6.6	2045	18	US-10-425-114-26238	Sequence 26238, A
42	46	6.6	2770	20	US-10-737-450-103	Sequence 103, App
43	46	6.6	3302	15	US-10-037-270-475	Sequence 475, App
44	46	6.6	3302	17	US-10-117-722-475	Sequence 475, App
45	46	6.6	3895	19	US-10-618-941-26	Sequence 26, Appli

ALIGNMENTS

RESULT 1

US-10-622-407-9  
; Sequence 9, Application US/10622407  
; Publication No. US20040018544A1  
; GENERAL INFORMATION:  
; APPLICANT: Saris, Chris  
; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL  
; FILE REFERENCE: 01017/35434B  
; CURRENT APPLICATION NUMBER: US/10/622,407  
; CURRENT FILING DATE: 2003-07-17  
; PRIOR APPLICATION NUMBER: US 09/612,033  
; PRIOR FILING DATE: 2000-07-07  
; PRIOR APPLICATION NUMBER: US 60/143,063  
; PRIOR FILING DATE: 1999-07-09  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 702  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (13)..(552)  
; FEATURE:  
; OTHER INFORMATION: Primer 2086-39  
US-10-622-407-9

Query Match 100.0%; Score 702; DB 17; Length 702;  
Best Local Similarity 100.0%; Pred. No. 7.1e-211;







Qy 501 TGTGTGCAGTTCATCTGTTCAA 523  
Db 462 TGTGTGCAGTTCATCTGTTCAA 484

## RESULT 8

US-09-855-266A-3  
; Sequence 3, Application US/09855266A  
; Patent No. US20020128435A1  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501-040002  
; CURRENT APPLICATION NUMBER: US/09/855,266A  
; CURRENT FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 09/411,722  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1509  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (12)...(539)  
US-09-855-266A-3

Query Match 53.8%; Score 377.4; DB 9; Length 1509;  
Best Local Similarity 90.7%; Pred. No. 4.4e-108;  
Matches 402; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 81 GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGCTAGTGAATT 140  
Db 50 GTTCTCTTCTGCTGCTGCTGAATCTGTTCTTCCGGTAATATTTGCTAGCTGAATC 109  
Qy 141 ACATCTCTTCAATGTCCCGCTGTGTAATCTGTCTTAAGACGTCTGTTCGCAAGACTG 200  
Db 110 ATACTCTTCAACTGTCCCGATGTGTAATCAAGTCTTAATGATGCTGTTCGCAAGACTG 169  
Qy 201 TTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAATCCCCATCTCAAGGACAATGTA 260  
Db 170 TCCCTCAGGTACATTTGTCAAGGCGCCCTGCGAATCCCCATCTCAAGGACAATGTA 229  
Qy 261 GAAGTGTCAACCCAGGAACATTCACAGGAAAGATAATTAATCTGATGCTGTGATCTTTG 320  
Db 230 GAAGTGTCAACCCAGGAACATTCACAGGAAAGATAATTAATGCTGATGCTGTGATCTTTG 289  
Qy 321 CTCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGCTCAGCCACCAAGTACCGGAA 380  
Db 290 CTCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGCTCAGCCACCAAGTACCGGAA 349  
Qy 381 ATGCAGTGGCGAAGCTCTTTACTACTATGACCCAAAATTTCCAGAAATCGTCCGCC 440  
Db 350 ATGGAGTGGCGAAGCTCTTTACTACTATGACCCAAAATTTCCAGAAATCATGCCGCC 409  
Qy 441 ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACAGCTAACAC 500  
Db 410 ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACAGCTAACAC 469  
Qy 501 TGTGTGCAGTTCATCTGTTCAA 523  
Db 470 TGTGTGCAGTTCATCTGTTCAA 492

## RESULT 9

US-10-802-332-3

; Sequence 3, Application US/10802332  
; Publication No. US20040152879A1  
; GENERAL INFORMATION:  
; APPLICANT: Kimura, Naoki  
; APPLICANT: Toyoshima, Tomoko  
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN  
; FILE REFERENCE: 06501-040002  
; CURRENT APPLICATION NUMBER: US/10/802,332  
; CURRENT FILING DATE: 2004-03-16  
; PRIOR APPLICATION NUMBER: US/09/855,266  
; PRIOR FILING DATE: 2001-05-14  
; PRIOR APPLICATION NUMBER: US 09/411,722  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: PCT/JP98/01511  
; PRIOR FILING DATE: 1998-04-01  
; PRIOR APPLICATION NUMBER: JP 9/099653  
; PRIOR FILING DATE: 1997-04-01  
; NUMBER OF SEQ ID NOS: 13  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 1509  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (12)...(539)  
US-10-802-332-3

Query Match 53.8%; Score 377.4; DB 19; Length 1509;  
Best Local Similarity 90.7%; Pred. No. 4.4e-108;  
Matches 402; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

Qy 81 GCTGCTGCTGCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGCTAGTGAATT 140  
Db 50 GTTCTCTTCTGCTGCTGCTGAATCTGTTCTTCCGGTAATATTTGCTAGCTGAATC 109  
Qy 141 ACATCTCTTCAATGTCCCGCTGTGTAATCTGTCTTAAGACGTCTGTTCGCAAGACTG 200  
Db 110 ATACTCTTCAACTGTCCCGATGTGTAATCAAGTCTTAATGATGCTGTTCGCAAGACTG 169  
Qy 201 TTCTGCAGGTACATTTGTCAAGGCGCCCTGCGAATCCCCATCTCAAGGACAATGTA 260  
Db 170 TCCCTCAGGTACATTTGTCAAGGCGCCCTGCGAATCCCCATCTCAAGGACAATGTA 229  
Qy 261 GAAGTGTCAACCCAGGAACATTCACAGGAAAGATAATTAATCTGATGCTGTGATCTTTG 320  
Db 230 GAAGTGTCAACCCAGGAACATTCACAGGAAAGATAATTAATGCTGATGCTGTGATCTTTG 289  
Qy 321 CTCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGCTCAGCCACCAAGTACCGGAA 380  
Db 290 CTCACCTGTGATAAAGATCAGGAAATGGTGGCGACTGCTCAGCCACCAAGTACCGGAA 349  
Qy 381 ATGCAGTGGCGAAGCTCTTTACTACTATGACCCAAAATTTCCAGAAATCGTCCGCC 440  
Db 350 ATGGAGTGGCGAAGCTCTTTACTACTATGACCCAAAATTTCCAGAAATCATGCCGCC 409  
Qy 441 ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACAGCTAACAC 500  
Db 410 ATGTACCAAGTGTCCCAAGGAATCCCTGTCTCCAGGAATGCAACTCCACAGCTAACAC 469  
Qy 501 TGTGTGCAGTTCATCTGTTCAA 523  
Db 470 TGTGTGCAGTTCATCTGTTCAA 492

## RESULT 10

US-10-193-616-5  
; Sequence 5, Application US/10193616  
; Publication No. US20030096355A1  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Ke  
; TITLE OF INVENTION: Isolation, Identification, and Characterization of  
; TITLE OF INVENTION: ymk25, a novel

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US-09-908-975-28273

Query Match      8.6%; Score 60.2; DB 10; Length 65;
Best Local Similarity 95.4%; Pred. No. 1.7e-08;
Matches 62; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY   567 AGATCCAGAAACCGCTGTTCCTACTGTTTATCACCTTGAGTAGTGTGTAATTGGTCCGT 626
     |||||
Db    1 AGATCCAGAAACCGCTGTCTCCTACTGTTATCACTTTGAGTGTGCTAATTGTGCCGT 60
     |||||

QY   627 TGTGTG 631
     |||
Db    61 GSTGG 65

RESULT 12
US-10-198-846-11546/c
; Sequence 11546, Application US/10198846
; Publication No. US2003099974A1
; GENERAL INFORMATION:
; APPLICANT: Lilie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steimann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11546
; LENGTH: 4248
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-198-846-11546

Query Match      6.9%; Score 48.4; DB 14; Length 4248;
Best Local Similarity 60.8%; Pred. No. 0.00078;
Matches 79; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY   20 GCCTCTTCTGCACGTGGTGTCCAGTCTGAGTCGGCTTCTTTGGCGCGGCTGCTGC 79
Db   1055 GTGCTTAAGGAGAACCAATTGAAGTCTGATTTGAGTGTGCTGCTGCTGCTGCTGC 996

QY   80 TGCTGCTGCTGCTGCTGCTGCTGAAATCTGCCCTTGCAAGGATAAAATTTGCTATGCTAGAAT 139
Db   995 TGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTCATGAGT 936

QY   140 TACAATCTCTT 149
Db   935 TTGGCCCCTTT 926

RESULT 13
US-10-489-372-43/c
; Sequence 43, Application US/10489372
; Publication No. US20040203014A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HONCHELL, Cynthia D.
; APPLICANT: WARREN, Bridget A.
; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: GRIPPIN, Jennifer A.
; APPLICANT: LI, Joana X.
; APPLICANT: LEE, Soo Yeun
; APPLICANT: YUE, Henry
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: MARQUIS, Joseph P.
; APPLICANT: GIETZEN, Kimberly J.
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; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: TRAN, Uyen K.
; APPLICANT: LEHR-MASON, Patricia M.
; APPLICANT: TANG, Y. Tom
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: KABLE, Amy E.
; APPLICANT: CHANG, Hsin-Ru
; APPLICANT: KHARE, Reena
; APPLICANT: BECHA, Shanya D.
; APPLICANT: JIN, Pei
; APPLICANT: LEE, Sally
; TITLE OF INVENTION: NEUROTRANSMISSION-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1185 USN
; CURRENT APPLICATION NUMBER: US/10/489,372
; CURRENT FILING DATE: 2004-03-12
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/322,180
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/326,096
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/327,446
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/343,903
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 60/334,020
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/340,226
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/345,008
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/365,645
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: US 60/379,887
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PERL Program
; SEQ ID NO 43
; LENGTH: 1269
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7505818CB1
US-10-489-372-43

Query Match      6.8%; Score 47.6; DB 20; Length 1269;
Best Local Similarity 66.7%; Pred. No. 0.00075;
Matches 68; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 18 TGGCTTCTTCGACGCTTGGTCCAGTCGAGTCGCTGCTCTCTTTGGCGGGGCTGCT 77
Db 901 TGGCTGCCCTTTCACATGGAATGGAATCTGCTGATAGTCCCTGCTGCTGCTGCT 842

Qy 78 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119
Db 841 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 800

RESULT 14
US-10-489-372-44/c
; Sequence 44, Application US/10489372
; Publication No. US20040203014A1
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: HONCHELL, Cynthia D.
; APPLICANT: WARREN, Bridget A.

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; APPLICANT: BOROWSKY, Mark L.
; APPLICANT: GRIFFIN, Jennifer A.
; APPLICANT: LI, Joana X.
; APPLICANT: LEE, Soo Yeun
; APPLICANT: YUE, Henry
; APPLICANT: FORSYTHE, Ian J.
; APPLICANT: MARQUIS, Joseph P.
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: TRAN, Uyen K.
; APPLICANT: LEHR-MASON, Patricia M.
; APPLICANT: TANG, Y. Tom
; APPLICANT: RAMKUMAR, Jayalaxmi
; APPLICANT: EMERLING, Brooke M.
; APPLICANT: LEE, Ernestine A.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: KABLE, Amy E.
; APPLICANT: CHANG, Hsin-Ru
; APPLICANT: KHARE, Reena
; APPLICANT: BECHA, Shanya D.
; APPLICANT: JIN, Pei
; APPLICANT: LEE, Sally
; TITLE OF INVENTION: NEUROTRANSMISSION-ASSOCIATED PROTEINS
; FILE REFERENCE: PF-1185 USN
; CURRENT APPLICATION NUMBER: US/10/489,372
; CURRENT FILING DATE: 2004-03-12
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: US 60/322,180
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 60/326,096
; PRIOR FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: US 60/327,446
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: US 60/345,837
; PRIOR FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 60/343,903
; PRIOR FILING DATE: 2001-11-27
; PRIOR APPLICATION NUMBER: US 60/334,020
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/340,226
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: US 60/345,008
; PRIOR FILING DATE: 2002-01-04
; PRIOR APPLICATION NUMBER: US 60/365,645
; PRIOR FILING DATE: 2002-03-18
; PRIOR APPLICATION NUMBER: US 60/379,887
; PRIOR FILING DATE: 2002-05-10
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PERL Program
; SEQ ID NO 44
; LENGTH: 1423
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7505821CB1
US-10-489-372-44

Query Match      6.8%; Score 47.6; DB 20; Length 1423;
Best Local Similarity 66.7%; Pred. No. 0.0008;
Matches 68; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

Qy 18 TGGCTTCTTCGACGCTTGGTCCAGTCGAGTCGCTGCTGCTCTTTGGCGGGGCTGCT 77
Db 985 TGGCTGCCCTTTCACATGGAATGGAATCTGCTGATAGTCCCTGCTGCTGCTGCT 925

Qy 78 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 119
Db 925 GCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 884

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		6.8%;	Score 47.6;	DB 9;	Length 2224;		
		Best Local Similarity	62.7%;	Pred. No.	0.001;		
		Matches	74;	Conservative	0;		
			Mismatches	44;	Indels	0; Gaps	0;
Qy	2	TGCACTCGGCCCATTTTGGCTTCCTTCGCAGCTTGGTGTCCAGTCTCAGTGTGCTGCTGCTCC	61				
Dd	309	TGCAACAGACCAGATGGACAACCTGGCTCTGGAGTTGGGCAAGCTAGGCAAGGGGTGC	250				
Qy	62	TTTGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGAATCTGCCTTTGCAGGT	119				

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 8, 2005, 13:43:46 ; Search time 8202.37 Seconds  
(without alignments)  
3257.733 Million cell updates/sec

Title: US-10-622-407-9  
Perfect score: 702  
Sequence: 1 ttgcacgcgcgatgttgg.....ttttattgtatgaagtgat 702

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: gb\_est1.\*  
2: gb\_est2.\*  
3: gb\_hic.\*  
4: gb\_est3.\*  
5: gb\_est4.\*  
6: gb\_est5.\*  
7: gb\_est6.\*  
8: gb\_ges1.\*  
9: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	697	99.3	2276	3 AK012838	AK012838 Mus muscu
2	694	98.9	1003	6 BY711952	BY711952 BY711952
3	602	85.8	765	7 CN461442	CN461442 UI-M-HB0-
4	602	85.8	4224	3 BC076592	BC076592 Mus muscu
5	573.4	81.7	696	5 BU611594	BU611594 UI-M-F10-
6	571	81.3	708	6 CB525851	CB525851 UI-M-FY0-
7	562	80.1	784	6 CB723050	CB723050 UI-M-GH0-
8	539	76.8	683	7 CF729486	CF729486 UI-M-HD0-
9	403	57.4	410	9 CG651536	CG651536 OST412784
10	382.4	55.9	415	9 CS535649	CS535649 OST122794
11	375.8	53.5	639	4 BG077775	BG077775 H3019F06-
12	358.8	51.1	585	2 BB613091	BB613091 BB613091
13	354.6	50.5	614	7 CN687949	CN687949 E0250A07-
14	353.6	50.4	597	7 CN697902	CN697902 E0401A05-
15	316.4	45.1	371	5 BY182663	BY182663 BY182663
16	315.8	45.0	489	7 CK333918	CK333918 H8266002-
17	304.2	43.3	331	5 BY343934	BY343934 BY343934
18	301	42.9	351	5 BY208766	BY208766 BY208766
19	295	42.0	317	5 BY345556	BY345556 BY345556
20	278.4	39.7	410	5 BY183172	BY183172 BY183172
21	266.4	37.9	331	5 BY195969	BY195969 BY195969
22	233.4	33.2	346	5 BY010018	BY010018 BY010018
23	232.8	33.2	347	2 BB873121	BB873121 BB873121
24	229.4	32.7	341	5 BY036522	BY036522 BY036522

25	223	31.8	338	5	BY325940	BY325940
26	210	29.9	544	1	AI747041	AI747041
27	208.2	29.7	320	5	BY181385	BY181385
28	208.2	29.7	333	5	BY175331	BY175331
29	208.2	29.7	340	5	BY187354	BY187354
30	208.2	29.7	355	5	BY177525	BY177525
31	193	27.5	296	5	BY142271	BY142271
32	190.2	27.1	235	7	CN688320	CN688320
33	189.2	27.0	210	7	CK342400	CK342400
34	181.4	25.8	403	5	BY201915	BY201915
35	152.8	21.8	664	6	CD469537	CD469537
36	119.4	17.0	607	8	AQ927517	AQ927517
37	110.4	15.7	599	8	AZ405040	AZ405040
38	102	14.5	756	7	CK634366	CK634366
39	94.8	13.5	763	9	AG478921	AG478921
40	91	13.0	709	9	BX969828	BX969828
41	87	12.4	742	6	C82050	C82050
42	87	12.4	900	6	C82250	C82250
43	86	12.3	741	1	AU050103	AU050103
44	85.4	12.2	747	1	AU050106	AU050106
45	80.4	11.5	719	6	BY748342	BY748342

ALIGNMENTS

RESULT 1  
LOCUS AK012838 2276 bp mRNA linear HTC 03-APR-2004  
DEFINITION Mus musculus 10, 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2810028K06 product:Tumor necrosis factor receptor superfamily member 21, full insert sequence.

ACCESSION AK012838  
VERSION AK012838.1 GI:12849843  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1  
AUTHORS Carninci,P. and Hayashizaki,Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 303, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636

REFERENCE 2  
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh M., Konno H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159

REFERENCE 3  
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoaka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishik,K., Kiteunai,T., Tashiro,H., Itoh,M., Sumi.N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamanoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaka,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861

REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research







[illegible]



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QY TGCCGAACAGGCTTTTACTACTATGACCCAAATTTCCAGAAATCGTGGCGCCATGTACC 447
Db TGCCGAACAGGCTTTTACTACTATGACTCAAAATTTCCAGAAATCGTGGCGCCATGTACC 420
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Db AGTTTCATCTGTTTCAA----- 496
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Db -ATCCGAAACCGGCTGTCTACTGTATATCACCCTTTGAGTGTGCTAAATTTGTGCCGTT 555
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QY TTGCTATGAAGTGAT 702
Db TTGCTATGAAGTGAT 630

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## RESULT 6

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CB525851
LOCUS CB525851 708 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-FY0-cfe-p-15-0-UI.r1 NIH BMAP_FY0 Mus musculus cDNA clone
IMAGE:6848608 5', mRNA sequence.

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## ACCESSION

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CB525851

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## VERSION

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CB525851.1 GI:29359322

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## KEYWORDS

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EST.

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## SOURCE

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Mus musculus (house mouse)

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## REFERENCE

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 708)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov

```

## AUTHORS

```

cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mousefl.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

```

## TITLES

```

The following repetitive elements were found in this cDNA
sequence: 35-71, >(CAG)n#simple_repeat (matched complement)
643-670, >(TAAA)n#simple_repeat (matched complement)
Seq primer: pYX-5.

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## FEATURES

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source
Location/Qualifiers
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/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="IMAGE:6848608"
/tissue_type="whole brain"
/dev_stage="embryo 13.5, 14.5, 15.5, 16.5, 17.5dpc"
/lab_host="DH10B (TI phage resistant)"
/clone_lib="NIH BMAP_FY0"
/notes="Organ: Brain; Vector: pYX- Asc; Site 1: EcOR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose

```

gel. First strand cDNA synthesis was primed with oligo-dT primer containing a Not I site. Double strand cDNA was size selected according to mRNA size fraction, ligated with EcoR I adaptor, digested with NotI and then cloned directionally into pYX-Asc vector. The library tag sequence located between the Not I site and the polyA tail is AGCAGACAG. This library was created for the University of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the Developing Mouse Nervous System', supported by National Institute of Mental Health (NIMH), Hemin Chin, Ph.D., program coordinator."

## ORIGIN

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Query Match 81.3%; Score 571; DB 6; Length 708;
Best Local Similarity 93.3%; Pred. No. 1.9e-154;
Matches 626; Conservative 0; Mismatches 0; Indels 45; Gaps 1;
QY 32 GCTTGGTGTCCAGTCTGAGTGGCTGCTCTTTGGCGCGGCTGCTGCTGCTGCTGTC 91
Db 1 GCTTGGTGTCCAGTCTGAGTGGCTGCTCTTTGGCGCGGCTGCTGCTGCTGCTGTC 60
QY 92 TGCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGCTATGCTAGAAATTACACTCCTTCA 151
Db 61 TGCTGCTGCTGAATCTGCCCTTGCAGGTAAATTTGCTATGCTAGAAATTACACTCCTTCA 120
QY 152 AATGTCCTGGTGTGAATACGTCTAAAGACGCTGTTGCAAGAACTGTTTCTGCAGGTA 211
Db 121 AATGTCCTGGTGTGAATACGTCTAAAGACGCTGTTGCAAGAACTGTTTCTGCAGGTA 180
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Db 181 CATTGTCAAGGCGCCCTGCGAATCCCATCTACTCAAGACATGTGAGAGTGTCCACC 240
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QY 332 ATAAAGATCAGGAAATGGTGGCCGACTGCTGACGACCAAGTGCAGGAAATGCCAGTGCC 391
Db 301 ATAAAGATCAGGAAATGGTGGCCGACTGCTGACGACCAAGTGCAGGAAATGCCAGTGCC 360
QY 392 GACAGCTCTTTACTACTATGACCCCAAAATTTCCAGAACTGTCGCCGCCATGTACCAAGT 451
Db 361 GACAGCTCTTTACTACTATGACCCCAAAATTTCCAGAACTGTCGCCGCCATGTACCAAGT 420
QY 452 GTCCCCAAGGAATCCCTGTCTCTCCAGGAATGCAACTCCACAGCTTAACACTGTGTGCAGTT 511
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QY 512 CATCTGTTTCAAGAAGATATGCTCCTCAGTGGCGCTTCTGAATGGTTTCACAGAGATC 571
Db 481 CATCTGTTTCAA-----ATC 495
QY 572 CCAGAAACCGGCTGCTCTACTGTTATCACTTTGAGTGTGCTAATTTGTCGCTGTTG 631
Db 496 CCAGAAACCGGCTGCTCTACTGTTATCACTTTGAGTGTGCTAATTTGTCGCTGTTG 555
QY 632 TCTTCCGTTATCATAAGAAGATAAAGGTTCTACAGATGTTTCTTAGCTTCTTTATGTC 691
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QY 692 TATGAAGTGAT 702
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## RESULT 7

```

CB723050
LOCUS CB723050 784 bp mRNA linear EST 09-JUL-2003
DEFINITION UI-M-GH0-cel-e-02-0-UI.r1 NIH BMAP_GH0 Mus musculus cDNA clone
IMAGE:6841035 5', mRNA sequence.
ACCESSION CB723050
VERSION CB723050.1 GI:29780192

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High quality sequence stop: 597

POLYA=No.

## FEATURES

source

Location/Qualifiers

1..597

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="E0401A05-5"

/clone="NIA:E0401A05 IMAGE:30868612"

/tissue type="whole embryo including extraembryonic

tissues" at 11.5-days postcoitum"

/dev\_stage="E11.5"

/lab\_host="DH10B"

/clone\_lib="NIA Mouse E11.5 whole embryo cDNA library

(long)"

/note="Vector: pCMV-SPORT6 (Invitrogen); Site 1: SalI;

Site 2: NotI; Mouse cDNA project by the Laboratory of Genetics, National Institute on Aging (NIA), Intramural Research Program, NIH (<http://igsun.grc.nia.nih.gov/cDNA>). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAs were extracted from a pool of 3 embryos at 11.5-days postcoitum. Double-stranded cDNAs were synthesized with an Oligo(dT) primer [Invitrogen]:

5'-pGACTAGTCTAGATCGGAGCGCCCTTTTTTTTTTTT-3' from 2ug of total RNA, treated with T4 DNA polymerase, and purified by ethanol-precipitation. The cDNAs were ligated to Lona-linker Lu-Sal4, purified by phenol/chloroform, and separated from free linkers by Centricon 100. Then, the cDNAs were amplified by long-range high fidelity PCR using Ex Taq polymerase (Takara) with a primer Sal4-S. The products were purified by phenol/chloroform and Centricon 100. The cDNAs were digested with SalI and NotI enzymes and cloned into SalI/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 3.3Kb. The library was constructed by Yulan Piao."

## ORIGIN

Query Match 50.4%; Score 353.6; DB 7; Length 597;  
 Best Local Similarity 91.7%; Pred. No. 2.8e-91;  
 Matches 374; Conservative 0; Mismatches 34; Indels 0; Gaps 0;

QY 116 AGGTAAATTTGCTATGCTAGAAATACACTCTTCAAAATGTCGCTGGTGAATACGTGT 175  
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 Db 97 AGGTAATATTGCTATGCTGAATCATACTCTTCAACTGTCGCTGGTGAATACCACT 156  
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QY 176 CTAAGAGCTGTGTTGCAAGAACTGTTCTGAGGTACATTTGTCAGGCGGCTGCGAAA 235  
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Db 157 CTAATGATGTCTGTTGCAAGAACTGTCGCTCAGGTACATTTGTCAGGCGGCTGCAAAA 216  
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QY 236 TCCCCATACCAAGGCAATGTGAGAGTGTACCCAGGACATTCACAGAGAAAGATA 295  
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Db 217 TCCCCATACCAAGGCAATGTGAGAGTGTACCCAGGACATTCACAGGAAAGATA 276  
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QY 296 ATTACTCGATGCTTGTATCTTTCTCCACTGTGATAAAGATCAGGAAATGTTGGCGG 355  
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QY 336 ACTGCTCAGCCACAGTACCGGAAATGCGAGTGCAGCAAGCTTTTACTATATGACC 415  
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Db 337 ACTGTTCTGCCACAGTACCGGAAATGCGAGTGCAGCAATAGGCTTTTACTATATGACC 396  
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QY 416 CAATATTTCCGAATGTCGCGCCCATGTACCAAGTGTCCCAAGGAATCCTGTCCTCC 475  
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Db 397 CAATATTTCCGAATGTCGCGCCCATGTACCAAGTGTCCCAAGGAATCCTGTCCTCC 456  
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QY 476 AGGAATGCAACTCCACAGTAACTGTTGAGTTCATCTGTTTCAA 523  
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Db 457 AGGAATGCAACTCCACAGTAACTGTTGAGTTCATCTGTTTCAA 504  
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## RESULT 15

BY182663

LOCUS

DEFINITION

BY182663 371 bp mRNA linear EST 10-DEC-2002  
 BY182663 RIKEN full-length enriched, NOD-derived CD11c +ve  
 dendritic cells Mus musculus cDNA clone F630103C16 5', mRNA  
 sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

BY182663.1 GI:26319309  
 EST.  
 Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 371)

REFERENCE

AUTHORS

Nikaido, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S.,  
 Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A.,  
 Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D.P., Bult, C.,  
 Hume, D.A., Quackenbush, J., Schriml, L.M., Kanapin, A., Matsuda, H.,  
 Batalov, S., Beisel, K.W., Blake, J.A., Bradt, D., Brusio, V.,  
 Ciochia, C., Corbani, L.E., Cousins, S., Dalla, E., Dragani, T.A.,  
 Fletcher, C.F., Forrest, A., Frazer, K.S., Gaasterland, T.,  
 Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S.,  
 Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E.D., Kanai, A.,  
 Kawaj, H., Kawasawa, Y., Kedzierzki, R.M., King, B.L., Kongsaya, A.,  
 Kurochkin, I.V., Lee, Y., Lenhard, B., Lyons, P.A., Maglott, D.R.,  
 Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T.,  
 Numata, K., Okido, T., Pavan, W.J., Pertea, G., Pesole, G.,  
 Petrovsky, N., Pillai, R., Pontius, J.U., Qi, D., Ramachandran, S.,  
 Ravasi, T., Reed, J.C., Reed, D.J., Reid, J., Ring, B.Z., Ringwald, M.,  
 Sandelin, A., Schneider, C., Semple, C.A., Setou, M., Shimada, K.,  
 Sultana, R., Takenaka, Y., Taylor, M.S., Teasdale, R.D., Tomita, M.,  
 Verardo, R., Wagner, L., Wahlestedt, C., Wang, Y., Watanabe, Y.,  
 Wells, C., Wilming, L.G., Wyshaw-Boris, A., Yanagisawa, M., Yang, I.,  
 Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P.,  
 Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M.,  
 Sakazume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K.,  
 Arakawa, T., Fukuda, S., Hara, A., Hashizume, W., Imotani, K., Ishii, Y.,  
 Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Sasaki, D., Shibata, K.,  
 Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E.S.,  
 Rogers, J., Birney, E. and Hayashizaki, Y.  
 Analysis of the mouse transcriptome based on functional annotation  
 of 60,770 full-length cDNAs  
 Nature 420, 563-573 (2002)  
 22354683  
 12466851

## TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
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 Fax: 81-45-503-9216

Email: genome-res@gsc.riken.jp, URL: <http://genome.gsc.riken.jp/>  
 Arakawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S.,  
 Hirozane, T., Imotani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H.,  
 Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R.,  
 Ohno, M., Sakai, K., Sakazume, N., Sasaki, D., Sato, K., Shibata, K.,  
 Shiraki, T., Tagami, M., Waki, K., Watahiki, A., Muramatsu, M. and  
 Hayashizaki, Y. Direct Submission  
 Computational Analysis of Full-Length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)

Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 cDNA library was prepared and sequenced in Mouse Genome



Search completed: September 9, 2005, 06:50:11  
Job time : 8205.37 secs



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10	208.5	20.7	355	1	US-08-292-549-6	Sequence 6, Appl	
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24	203.5	20.2	336	4	US-09-756-186-8	Sequence 8, Appl	
25	202.5	20.1	199	1	US-08-050-319B-48	Sequence 48, Appl	
26	202.5	20.1	199	2	US-08-465-982-48	Sequence 48, Appl	
27	201.5	20.0	167	1	US-08-050-319B-2	Sequence 2, Appl	

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; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-612-033B-8

Query Match          94.8%; Score 956; DB 4; Length 198;
Best Local Similarity 100.0%; Pred. No. 6.9e-83;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 121 DRKQCRRTGLYYDPKPEPCRCCTKCPQGPVLQECNSTANTVCSSTS 170
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RESULT 3
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; Sequence 14, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmat2, a No. 6627199el Member of the TNF-Receptor Superfamily
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
; OTHER INFORMATION: consisting of Mus musculus sequences and
; OTHER INFORMATION: immunoglobulin sequences
US-09-612-033B-14

Query Match          94.8%; Score 956; DB 4; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.5e-82;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATS 120
Db 61 KNCAGTFVAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRRTGLYYDPKPEPCRCCTKCPQGPVLQECNSTANTVCSSTS 170
Db 121 DRKQCRRTGLYYDPKPEPCRCCTKCPQGPVLQECNSTANTVCSSTS 170

RESULT 4
US-09-612-033B-6
```

```
; Sequence 6, Application US/09612033B
; Patent No. 6627199
; GENERAL INFORMATION:
; APPLICANT: Sarris, Chris
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: tmat2, a No. 6627199el Member of the TNF-Receptor Superfamily
; FILE REFERENCE: 01017/35434A
; CURRENT APPLICATION NUMBER: US/09/612,033B
; CURRENT FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,063
; PRIOR FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-612-033B-6

Query Match          74.2%; Score 748; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 2.1e-63;
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60

Qy 61 KNCAGTFVAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATS 120
Db 61 KNCAGTFVAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATS 120

Qy 121 DRKQCRRTGLYY 133
Db 121 DRKQCRRTGLYY 133

RESULT 5
US-09-411-722-1
; Sequence 1, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501/040001
; CURRENT APPLICATION NUMBER: US/09/411,722
; CURRENT FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-1

Query Match          69.9%; Score 705; DB 3; Length 176;
Best Local Similarity 79.9%; Pred. No. 3.3e-59;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

Qy 7 SLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCSAG 66
Db 5 SHVSSLSHWF-----LLLLLLLLLPLVIFAMPESYSEFCPDGGEYQSDNDVCCCTCPG 56

Qy 67 TFVKAPCEIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATSDRKQC 126
Db 57 TFVKAPCKIPHTQGCCEKCHPGTFTKDNLYLDACILCSTCDKQNMVADCSATSDRKCEC 116

Qy 127 RTGLYYDPKPEPCRCCTKCPQGPVLQECNSTANTVCSSTS 170
```

```

Db      117 QIGLYYDYPKPPESCRPTKCPQIGIPVLQECNSTANTVCSSTS 160
: |||||
RESULT 6
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; PRIOR FILING DATE: 2001-05-14
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1997-04-01
; PRIOR FILING DATE: 1997-04-01
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-1

Query Match      69.9%; Score 705; DB 4; Length 176;
Best Local Similarity 79.9%; Pred. No. 3.3e-59;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY      7 SLVSSSRWFLRLLLLLLLLNLPQVKFAMLEHSPKCPAGEYWSKDVCKKNCAG 66
: |||||
Db      5 SHVSSLSHWF-----LRLLLNLPVIFAMPESIFNCPDGETQSDNVCKTCPSG 56
: |||||

QY      67 TFVKAPCEIPHTQOCEKCHPGFTTEKNDYLDACILGSTCDKQEMVADCSATSDRKQC 126
: |||||
Db      57 TFVKAPCKIPHTQOCEKCHPGFTTGKNGHLDCELSTCDKQNMVADCSATSDRKCEC 116
: |||||

QY      127 RTGLYYDYPKPPESCRPTKCPQIGIPVLQECNSTANTVCSSTS 170
: |||||
Db      117 QIGLYYDYPKPPESCRPTKCPQIGIPVLQECNSTANTVCSSTS 160
: |||||

RESULT 7
US-09-411-722-2
; Sequence 2, Application US/09411722
; Patent No. 6271366
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501/040001
; CURRENT APPLICATION NUMBER: US/09/411,722
; CURRENT FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1998-04-01
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-411-722-2

Query Match      63.6%; Score 641; DB 3; Length 148;
Best Local Similarity 84.8%; Pred. No. 3.1e-53;
Matches 112; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY      39 AMLEHSPKCPAGEYWSKDVCKKNCAGTFVKAPCEIPHTQOCEKCHPGFTTEKNDYLD 98
: |||||
Db      1 AMPESYSFNCPEGEYQSDNVCKTCPSGTFVKAPCKIPHTQOCEKCHPGFTTGKNGHLH 60
: |||||

QY      99 ACILGSTCDKQEMVADCSATSDRKQCQRTGLYYDYPKPPESCRPTKCPQIGIPVLQECN 158
: |||||
Db      61 DCELCSTCDKQNMVADCSATSDRKCECQIGLYYDYPKPPESCRPTKCPQIGIPVLQECN 120
: |||||

QY      159 STANTVCSSTS 170
: |||||
Db      121 STANTVCSSTS 132
: |||||

RESULT 8
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1998-04-01
; PRIOR FILING DATE: 1997-04-01
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-2

Query Match      63.6%; Score 641; DB 4; Length 148;
Best Local Similarity 84.8%; Pred. No. 3.1e-53;
Matches 112; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY      39 AMLEHSPKCPAGEYWSKDVCKKNCAGTFVKAPCEIPHTQOCEKCHPGFTTEKNDYLD 98
: |||||
Db      1 AMPESYSFNCPEGEYQSDNVCKTCPSGTFVKAPCKIPHTQOCEKCHPGFTTGKNGHLH 60
: |||||

QY      99 ACILGSTCDKQEMVADCSATSDRKQCQRTGLYYDYPKPPESCRPTKCPQIGIPVLQECN 158
: |||||
Db      61 DCELCSTCDKQNMVADCSATSDRKCECQIGLYYDYPKPPESCRPTKCPQIGIPVLQECN 120
: |||||

QY      159 STANTVCSSTS 170
: |||||
Db      121 STANTVCSSTS 132
: |||||

RESULT 9
US-09-855-266A-13
; Sequence 13, Application US/09855266A
; Patent No. 6784284
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: 1998-04-01
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-13

Query Match      63.6%; Score 641; DB 3; Length 148;
Best Local Similarity 84.8%; Pred. No. 3.1e-53;
Matches 112; Conservative 5; Mismatches 15; Indels 0; Gaps 0;

QY      39 AMLEHSPKCPAGEYWSKDVCKKNCAGTFVKAPCEIPHTQOCEKCHPGFTTEKNDYLD 98
: |||||
Db      1 AMPESYSFNCPEGEYQSDNVCKTCPSGTFVKAPCKIPHTQOCEKCHPGFTTGKNGHLH 60
: |||||

QY      99 ACILGSTCDKQEMVADCSATSDRKQCQRTGLYYDYPKPPESCRPTKCPQIGIPVLQECN 158
: |||||
Db      61 DCELCSTCDKQNMVADCSATSDRKCECQIGLYYDYPKPPESCRPTKCPQIGIPVLQECN 120
: |||||

QY      159 STANTVCSSTS 170
: |||||
Db      121 STANTVCSSTS 132
: |||||
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-13

Query Match      21.1%; Score 212.5; DB 4; Length 123;
Best Local Similarity 34.7%; Pred. No. 8.4e-13;
Matches 43; Conservative 15; Mismatches 59; Indels 7; Gaps 4;

Qy 48 CPAGEY---NSKDVCKKNSAGTFAKPCETPHPTGQCEKCHPCGTFTKDNLYDACILCS 104
Db 1 CPQGYVHSKNSISCTCKCHKGTVLVSDCPSPGRDVTVCREKGTFTASQNYLRQCLUSCK 60

Qy 105 TCDKD--QEMVADCSATSDRKCQCRGTGLY--YDPKFPSPCRPCTKCPQGIPLVQECNSTA 161
Db 61 TCRKMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNG-TVTIPCKETQ 119

Qy 162 NTVC 165
Db 120 NTVC 123

RESULT 10
US-08-292-549-6
; Sequence 6, Application US/08292549
; Patent No. 5464938
; GENERAL INFORMATION:
; APPLICANT: Smith, Craig A.
; APPLICANT: Goodwin, Raymond G.
; TITLE OF INVENTION: Isolated Viral Protein TNF Antagonists
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/292,549
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/963,330
; FILING DATE: 10/19/92
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2602-A
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-292-549-6

Query Match      20.7%; Score 208.5; DB 1; Length 355;
Best Local Similarity 33.8%; Pred. No. 6.5e-12;
Matches 51; Conservative 21; Mismatches 68; Indels 11; Gaps 6;

Qy 21 LLLLLLLLLLPLQVKFAMLEHLSFKCPAGEYWSKDVCKKNSAGTFVKAPCEI-PHTQ 79
Db 1 LLLLLLLLLLPLQVKFAMLEHLSFKCPAGEYWSKDVCKKNSAGTFVKAPCEI-PHTQ 79

US-09-855-266A-13

Query Match      21.1%; Score 212.5; DB 4; Length 123;
Best Local Similarity 34.7%; Pred. No. 8.4e-13;
Matches 43; Conservative 15; Mismatches 59; Indels 7; Gaps 4;

Qy 48 CPAGEY---NSKDVCKKNSAGTFAKPCETPHPTGQCEKCHPCGTFTKDNLYDACILCS 104
Db 1 CPQGYVHSKNSISCTCKCHKGTVLVSDCPSPGRDVTVCREKGTFTASQNYLRQCLUSCK 60

Qy 105 TCDKD--QEMVADCSATSDRKCQCRGTGLY--YDPKFPSPCRPCTKCPQGIPLVQECNSTA 161
Db 61 TCRKMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNG-TVTIPCKETQ 119

Qy 162 NTVC 165
Db 120 NTVC 123

RESULT 11
US-09-006-353A-14
; Sequence 14, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 355 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-006-353A-14

Query Match      20.7%; Score 208.5; DB 3; Length 355;
Best Local Similarity 33.8%; Pred. No. 6.5e-12;
Matches 51; Conservative 21; Mismatches 68; Indels 11; Gaps 6;

Qy 21 LLLLLLLLLLPLQVKFAMLEHLSFKCPAGEYWSKDVCKKNSAGTFVKAPCEI-PHTQ 79
Db 7 LLLLLLLLLLPLQVKFAMLEHLSFKCPAGEYWSKDVCKKNSAGTFVKAPCEI-PHTQ 79

US-09-855-266A-13

Query Match      21.1%; Score 212.5; DB 4; Length 123;
Best Local Similarity 34.7%; Pred. No. 8.4e-13;
Matches 43; Conservative 15; Mismatches 59; Indels 7; Gaps 4;

Qy 48 CPAGEY---NSKDVCKKNSAGTFAKPCETPHPTGQCEKCHPCGTFTKDNLYDACILCS 104
Db 1 CPQGYVHSKNSISCTCKCHKGTVLVSDCPSPGRDVTVCREKGTFTASQNYLRQCLUSCK 60

Qy 105 TCDKD--QEMVADCSATSDRKCQCRGTGLY--YDPKFPSPCRPCTKCPQGIPLVQECNSTA 161
Db 61 TCRKMSQVEISPCQADKDTVCGCKENQFQRYLSETHFQCVDCSPCFNG-TVTIPCKETQ 119

Qy 162 NTVC 165
Db 120 NTVC 123

RESULT 12
US-09-573-986-14
```

Query Match 20.6%; Score 207.5; DB 3; Length 285;

Best Local Similarity 34.4%; Pred. No. 6.3e-12;  
Matches 53; Conservative 17; Mismatches 71; Indels 13; Gaps 6;  
Qy 20 RLLLLLLLLNLP-LQVKFAMLELHSPKCPAGY---WSKDVCCCKNCAGTFVKAPCEI 75  
Db 2 RLSLLAFGLLCLPWLQESA-----DSVCPQGYIHPQNNISICTKCHKGTLYLNDPCG 56  
Qy 76 PHTGQCEKCHPGTFTKDNVLDACILCSTCKD--QEMVADCSATSDRKQCQRTGLY-Y 132  
Db 57 PGQDTCRECESGSFTASENHLRCLSCSKCKRMGQVEISSCTVDRDVTGCKRKNQYRH 116  
Qy 133 YDPKFPESCRCPTCKPOGIPVLQECNSTANTVCS 166  
Db 117 YWSENLFQCFNCTLCCLNG-TVHLSCQEKQNTVCT 149

## RESULT 15

US-09-756-186-6  
; Sequence 6, Application US/09756186  
; Patent No. 6663867  
; GENERAL INFORMATION:  
; APPLICANT: Campbell, Robert K.  
; APPLICANT: Jameson, Bradford A.  
; APPLICANT: Chappel, Scott C.  
; TITLE OF INVENTION: HYBRID PROTEINS  
; NUMBER OF SEQUENCES: 22  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street N.W., Ste. 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 22207  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09756.186  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/804,166  
; FILING DATE:  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Browdy, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER: CAMPBELL=2A  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 628-5197  
; TELEFAX: (202) 737-3528  
; INFORMATION FOR SEQ ID NO: 6:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 285 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-756-186-6

Query Match 20.6%; Score 207.5; DB 4; Length 285;  
Best Local Similarity 34.4%; Pred. No. 6.3e-12;  
Matches 53; Conservative 17; Mismatches 71; Indels 13; Gaps 6;  
Qy 20 RLLLLLLLLNLP-LQVKFAMLELHSPKCPAGY---WSKDVCCCKNCAGTFVKAPCEI 75  
Db 2 RLSLLAFGLLCLPWLQESA-----DSVCPQGYIHPQNNISICTKCHKGTLYLNDPCG 56  
Qy 76 PHTGQCEKCHPGTFTKDNVLDACILCSTCKD--QEMVADCSATSDRKQCQRTGLY-Y 132  
Db 57 PGQDTCRECESGSFTASENHLRCLSCSKCKRMGQVEISSCTVDRDVTGCKRKNQYRH 116

Qy 133 YDPKFPESCRCPTCKPOGIPVLQECNSTANTVCS 166  
Db 117 YWSENLFQCFNCTLCCLNG-TVHLSCQEKQNTVCT 149  
Search completed: September 9, 2005, 09:35:54  
Job time : 117.19 secs



120

Qy 121 DRKQCRRTGLYYDPKPPESCRPCTKCPQGIPLVQECNSTANTVCSVSSVRSASVAVPI 180  
|  
Db 121 DRKQCRRTGLYYDPKPPESCRPCTKCPQGIPLVQECNSTANTVCSVSSVRSASVAVPI 180  
|

## RESULT 2

US-10-622-407-8

; Sequence 8, Application US/10622407

; Publication No. US20040018544A1

; GENERAL INFORMATION:

; APPLICANT: Saris, Chris

; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL

; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

; FILE REFERENCE: 01017/35434B

; CURRENT APPLICATION NUMBER: US/10/622,407

; CURRENT FILING DATE: 2003-07-17

; PRIOR APPLICATION NUMBER: US 09/612,033

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,063

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 8

; LENGTH: 198

; TYPE: PRT

; ORGANISM: Mus musculus

; US-10-622-407-8

Query Match 94.8%; Score 956; DB 15; Length 198;  
Best Local Similarity 100.0%; Pred. No. 2.5e-76;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
|

Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
|

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATS 120  
|

Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATS 120  
|

Qy 121 DRKQCRRTGLYYDPKPPESCRPCTKCPQGIPLVQECNSTANTVCSVSSVS 170  
|

Db 121 DRKQCRRTGLYYDPKPPESCRPCTKCPQGIPLVQECNSTANTVCSVSSVS 170  
|

## RESULT 3

US-10-622-407-14

; Sequence 14, Application US/10622407

; Publication No. US20040018544A1

; GENERAL INFORMATION:

; APPLICANT: Saris, Chris

; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NOVEL

; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

; FILE REFERENCE: 01017/35434B

; CURRENT APPLICATION NUMBER: US/10/622,407

; CURRENT FILING DATE: 2003-07-17

; PRIOR APPLICATION NUMBER: US 09/612,033

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,063

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 14

; LENGTH: 398

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Fusion protein

; OTHER INFORMATION: consisting of Mus musculus sequences and

; OTHER INFORMATION: immunoglobulin sequences

US-10-622-407-14

Query Match 94.8%; Score 956; DB 15; Length 398;  
Best Local Similarity 100.0%; Pred. No. 4.9e-76;  
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
|

Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
|

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATS 120  
|

Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATS 120  
|

Qy 121 DRKQCRRTGLYYDPKPPESCRPCTKCPQGIPLVQECNSTANTVCSVSSVS 170  
|

Db 121 DRKQCRRTGLYYDPKPPESCRPCTKCPQGIPLVQECNSTANTVCSVSSVS 170  
|

## RESULT 4

US-10-622-407-6

; Sequence 6, Application US/10622407

; Publication No. US20040018544A1

; GENERAL INFORMATION:

; APPLICANT: Saris, Chris

; TITLE OF INVENTION: ISOLATION, IDENTIFICATION, AND CHARACTERIZATION OF TMST2, A NO

; TITLE OF INVENTION: MEMBER OF THE TNF-RECEPTOR SUPERFAMILY OF GENES

; FILE REFERENCE: 01017/35434B

; CURRENT APPLICATION NUMBER: US/10/622,407

; CURRENT FILING DATE: 2003-07-17

; PRIOR APPLICATION NUMBER: US 09/612,033

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,063

; PRIOR FILING DATE: 1999-07-09

; NUMBER OF SEQ ID NOS: 15

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 133

; TYPE: PRT

; ORGANISM: Mus musculus

; US-10-622-407-6

Query Match 74.2%; Score 748; DB 15; Length 133;  
Best Local Similarity 100.0%; Pred. No. 3.6e-58;  
Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
|

Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
|

Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATS 120  
|

Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATS 120  
|

Qy 121 DRKQCRRTGLYY 133  
|

Db 121 DRKQCRRTGLYY 133  
|

## RESULT 5

US-10-193-616-14

; Sequence 14, Application US/10193616

; Publication No. US20030096355A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Ke

; TITLE OF INVENTION: Isolation, Identification, and Characterization of

; TITLE OF INVENTION: ymkz5, a novel

; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family

; FILE REFERENCE: 01017/35551A

; CURRENT APPLICATION NUMBER: US/10/193,616

; CURRENT FILING DATE: 2002-07-11

; PRIOR APPLICATION NUMBER: US/09/611,989

; PRIOR FILING DATE: 2000-07-07

; PRIOR APPLICATION NUMBER: US 60/143,137

; PRIOR FILING DATE: 1999-07-07

```
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: ymkz5-Fc fusion protein
US-10-193-616-14

Query Match          70.3%; Score 709; DB 14; Length 396;
Best Local Similarity 78.6%; Pred. No. 2.8e-54;
Matches 132; Conservative 6; Mismatches 22; Indels 8; Gaps 1;

QY 7 SLVSSLSRWFLWRLRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCAG 66
DB 5 SHVSSLSHWP-----LRLRLRLPLVIFAMPESYFNCNCPDGEYQSNVDCCKTSPG 56

QY 67 TFVKAPCEIPHTQOCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPESCRCPTKCPQIPVLQECNSTANTVCSSSVSRSA 174
DB 117 QIGLYYYDDPKFPESCRCPTKCPQIPVLQECNSTANTVCSSSVSNAAA 164

RESULT 6
US-09-855-266A-1
; Sequence 1, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; PRIOR FILING DATE: 2001-05-14
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR FILING DATE: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-1

Query Match          69.9%; Score 705; DB 9; Length 176;
Best Local Similarity 79.9%; Pred. No. 2.9e-54;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY 7 SLVSSLSRWFLWRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCAG 66
DB 5 SHVSSLSHWP-----LRLRLRLPLVIFAMPESYFNCNCPDGEYQSNVDCCKTSPG 56

QY 67 TFVKAPCEIPHTQOCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPESCRCPTKCPQIPVLQECNSTANTVCSSSVS 170
DB 117 QIGLYYYDDPKFPESCRCPTKCPQIPVLQECNSTANTVCSSSVS 160

RESULT 7
US-10-193-616-8
; Sequence 8, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; TITLE OF INVENTION: ymkz5, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616
; CURRENT FILING DATE: 2002-07-11
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 2000-07-07
; PRIOR FILING DATE: 1999-07-07
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-193-616-8

Query Match          69.9%; Score 705; DB 14; Length 176;
Best Local Similarity 79.9%; Pred. No. 2.9e-54;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY 7 SLVSSLSRWFLWRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCAG 66
DB 5 SHVSSLSHWP-----LRLRLRLPLVIFAMPESYFNCNCPDGEYQSNVDCCKTSPG 56

QY 67 TFVKAPCEIPHTQOCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPESCRCPTKCPQIPVLQECNSTANTVCSSSVS 170
DB 117 QIGLYYYDDPKFPESCRCPTKCPQIPVLQECNSTANTVCSSSVS 160

RESULT 8
US-10-802-332-1
; Sequence 1, Application US/10802332
; Publication No. US20040152879A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/10/802,332
; CURRENT FILING DATE: 2004-03-16
; PRIOR FILING DATE: 2001-05-14
; PRIOR FILING DATE: 1999-10-01
; PRIOR FILING DATE: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR FILING DATE: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 176
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-802-332-1

Query Match          69.9%; Score 705; DB 16; Length 176;
Best Local Similarity 79.9%; Pred. No. 2.9e-54;
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY 7 SLVSSLSRWFLWRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCAG 66
DB 5 SHVSSLSHWP-----LRLRLRLPLVIFAMPESYFNCNCPDGEYQSNVDCCKTSPG 56

QY 67 TFVKAPCEIPHTQOCEKCHPGTFTKDNVLDACILCSTCDKQEMVADCSATSDRKQC 126
DB 57 TFVKAPCKIPHTQOCEKCHPGTFTGKDNGLHDCELCSTCDKQNMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPESCRCPTKCPQIPVLQECNSTANTVCSSSVS 170
DB 117 QIGLYYYDDPKFPESCRCPTKCPQIPVLQECNSTANTVCSSSVS 160
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[illegible]

```

RESULT 9
US-09-855-266A-2
; Sequence 2, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 05/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 148
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-2

```

Query Match	63.6%;	Score 641;	DB 9;	Length 148;
Best Local Similarity	84.8%;	Pred. No. 1.1e-48;		
Matches 112;	Conservative 5;	Mismatches 15;	Indels 0;	Gaps 0;
QY	39	AMELHSEKPCAGEYMSKDVCKNCASAGTVFKAPCEIPTHTGOGCEKCHPGCTFTFKDNYLD	98	
Db	1	AMPESYSFNCPDGEYOSNDVCKTCSGTVFKAPCKIPTHTGOGCEKCHPGCTFTFKDNGLH	60	
QY	99	ACTLCSTCDKXQBMVADCSATSDRKCCOCTGLYYYDPKFPESCRCPTCKCQGIPIVLQECN	158	
Db	61	DCELCSTCDKXQNMVADCSATSDRKCECQIGLYYYDPKFPESCRCPTCKCQGIPIVLQECN	120	
QY	159	STANTVCSSSVS	170	
Db	121	STANTVCSSSVS	132	

```

QY / SLYSSLSRWFLWARKLELLLLLLLNTLPQVKFAMLELHSHFACPAGEIWSKDVUCCNLSAG 86
| | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | |
Db 5 SHVSSLSHWPF-----LLLLLLNLNLFPIFAMPESYSFNCPDGEYQSNDVCCCKTSPG 56
| | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | |
Qy 67 TFVKAPCEIPHTGOCEKECHPGFTFEKDNYLDACLSTCDKQEMVADCSATSDRKQC 126
| | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | |
Db 57 TFVKAPCKIPHTGOCEKECHPGFTTGKDXGLHDCELSTCDKQNMVADCSATSDRKQEC 116
| | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | |
Qy 127 R 127
| | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | |
Db 117 Q 117
| | | | | | | | | | | | | | | | : | | | | | | | | | | | | | | | |

RESULT 12
US-10-193-616-10
; Sequence 10, Application US/10193616
; Publication No. US20030096355A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Ke
; TITLE OF INVENTION: Isolation, Identification, and Characterization of
; ymkz5, a novel
; TITLE OF INVENTION: member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35551A
; CURRENT APPLICATION NUMBER: US/10/193,616

```

```
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: US/09/611,989
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/143,137
; PRIOR FILING DATE: 1999-07-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 10
; LENGTH: 247
; TYPE: PRT
; ORGANISM: Mus musculus
; FEATURE:
; OTHER INFORMATION: TNFRI
US-10-193-616-10

Query Match      21.6%; Score 217.5; DB 14; Length 247;
Best Local Similarity 32.3%; Pred. No. 3.6e-11;
Matches 51; Conservative 19; Mismatches .75; Indels 13; Gaps 5;

QY 21 LLLLLLLLLLNL-----PLQVKFAMLELHSPKCPAGEY---WSKDVCCCKNSAGTFVKA 71
DB 11 LSLVLLALLMGHPSGVTGLVPSLGDREKRDLSLCPQGYVHSHKNSICCTKCHKGTLYVS 70

QY 72 PCBPHTQGOCEKCHPGTFTTEKDYLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
DB 71 DCPSGRDVTVCRECKGTFTTASQNYLRQCLSCCTCKRMSQVEISPCQADKDTVCGCKEN 130

QY 130 LYY-YDPKFPESCPCCTKCPQGIPLVQECNSTANTVCS 166
DB 131 QFORYLSETHFQVDCSPCFNG-TVTIPCKETQNTVCN 167

RESULT 13
US-10-410-012-3
; Sequence 3, Application US/10410012
; Publication No. US20030228276A1
; GENERAL INFORMATION:
; APPLICANT: Pitossi, Fernando J
; APPLICANT: Eisell, Ulrich L M
; TITLE OF INVENTION: Neuroprotective and neurodegenerative effects of long-term expres
; FILE REFERENCE: 1418P US/101141-17
; CURRENT APPLICATION NUMBER: US/10/410,012
; CURRENT FILING DATE: 2003-04-09
; PRIOR APPLICATION NUMBER: US 60/370,974
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 3
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-410-012-3

Query Match      21.6%; Score 217.5; DB 15; Length 454;
Best Local Similarity 32.3%; Pred. No. 6.5e-11;
Matches 51; Conservative 19; Mismatches .75; Indels 13; Gaps 5;

QY 21 LLLLLLLLLLNL-----PLQVKFAMLELHSPKCPAGEY---WSKDVCCCKNSAGTFVKA 71
DB 11 LSLVLLALLMGHPSGVTGLVPSLGDREKRDLSLCPQGYVHSHKNSICCTKCHKGTLYVS 70

QY 72 PCBPHTQGOCEKCHPGTFTTEKDYLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
DB 71 DCPSGRDVTVCRECKGTFTTASQNYLRQCLSCCTCKRMSQVEISPCQADKDTVCGCKEN 130

QY 130 LYY-YDPKFPESCPCCTKCPQGIPLVQECNSTANTVCS 166
DB 131 QFORYLSETHFQVDCSPCFNG-TVTIPCKETQNTVCN 167

RESULT 14
US-10-799-345-24
```

```
; Sequence 24, Application US/10799345
; Publication No. US20040209316A1
; GENERAL INFORMATION:
; APPLICANT: Christopher T. Ritchlin
; APPLICANT: Sally Haas-Smith
; APPLICANT: Edward Schwarz
; TITLE OF INVENTION: Methods and Compositions Related to
; TITLE OF INVENTION: Joint Inflammation Diseases
; FILE REFERENCE: 21108.003102
; CURRENT APPLICATION NUMBER: US/10/799,345
; CURRENT FILING DATE: 2004-03-12
; PRIOR APPLICATION NUMBER: 60/454,573
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:/Note =
; OTHER INFORMATION: Synthetic Construct
US-10-799-345-24

Query Match      21.6%; Score 217.5; DB 16; Length 454;
Best Local Similarity 32.3%; Pred. No. 6.5e-11;
Matches 51; Conservative 19; Mismatches .75; Indels 13; Gaps 5;

QY 21 LLLLLLLLLLNL-----PLQVKFAMLELHSPKCPAGEY---WSKDVCCCKNSAGTFVKA 71
DB 11 LSLVLLALLMGHPSGVTGLVPSLGDREKRDLSLCPQGYVHSHKNSICCTKCHKGTLYVS 70

QY 72 PCBPHTQGOCEKCHPGTFTTEKDYLDACILCSTCDKD--QEMVADCSATSDRKCCQRTG 129
DB 71 DCPSGRDVTVCRECKGTFTTASQNYLRQCLSCCTCKRMSQVEISPCQADKDTVCGCKEN 130

QY 130 LYY-YDPKFPESCPCCTKCPQGIPLVQECNSTANTVCS 166
DB 131 QFORYLSETHFQVDCSPCFNG-TVTIPCKETQNTVCN 167

RESULT 15
US-09-855-266A-13
; Sequence 13, Application US/09855266A
; Patent No. US20020128435A1
; GENERAL INFORMATION:
; APPLICANT: Kimura, Naoki
; APPLICANT: Toyoshima, Tomoko
; TITLE OF INVENTION: NOVEL SECRETORY MEMBRANE PROTEIN
; FILE REFERENCE: 06501-040002
; CURRENT APPLICATION NUMBER: US/09/855,266A
; CURRENT FILING DATE: 2001-05-14
; PRIOR APPLICATION NUMBER: US 09/411,722
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: PCT/JP98/01511
; PRIOR FILING DATE: 1998-04-01
; PRIOR APPLICATION NUMBER: JP 9/099653
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-855-266A-13

Query Match      21.1%; Score 212.5; DB 9; Length 123;
Best Local Similarity 34.7%; Pred. No. 5e-11;
Matches 43; Conservative 15; Mismatches 59; Indels 7; Gaps 4;

QY 48 CPAGEY---WSKDVCCCKNSAGTFVKA PCBPHTQGOCEKCHPGTFTTEKDYLDACILCS 104
DB 1 CPGGYVHSHKNSICCTKCHKGTLYVSDCPSPGRDVTVCRECKGTFTTASQNYLRQCLSCCK 60
```



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 9, 2005, 06:50:20 ; Search time 130.476 Seconds  
(without alignments)  
132.737 Million cell updates/sec

Title: US-10-622-407-10

Perfect score: 1008

Sequence: 1 MFGFCSLVSLSRWFLMR.....ANTVCSSVSRSSASVAMPI 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:\*

1: piri:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	217.5	21.6	454	1 GQMST1	tumor necrosis fac
2	204.5	20.3	461	1 GQRTT1	tumor necrosis fac
3	201.5	20.0	348	2 T28623	hypothetical prote
4	201.5	20.0	349	2 D36858	gene G4R protein -
5	201.5	20.0	349	2 D72175	G2R protein - vari
6	201.5	20.0	455	1 GQHUT1	tumor necrosis fac
7	200.5	19.9	461	2 JC4302	tumor necrosis fac
8	188	18.7	271	2 S12783	OX40 antigen precu
9	188	18.7	324	2 JC2395	Fas antigen precu
10	188	18.7	427	1 GQHUN	nerve growth facto
11	183	18.2	327	2 A46484	apoptosis-mediatin
12	182	18.1	314	2 I37383	FAS soluble protei
13	180.5	17.9	651	2 JC7705	death receptor-6 -
14	180	17.9	335	2 A40036	apoptosis-mediatin
15	176.5	17.5	416	1 JN0006	nerve growth facto
16	175	17.4	425	1 A26431	nerve growth facto
17	173.5	17.2	461	1 A35356	tumor necrosis fac
18	173	17.2	325	2 B43692	T2 protein - rabbi
19	167.5	16.6	326	1 GQVZML	T2 protein - myxom
20	163.5	16.2	272	2 I48700	gene OX40 protein
21	157.5	15.6	260	1 A46517	CD27 antigen precu
22	154.5	15.3	474	2 B38634	tumor necrosis fac
23	150	14.9	459	2 I48854	gene murine tumour
24	150	14.9	595	2 A42086	CD30 antigen precu
25	149.5	14.8	250	1 A49053	CD27 antigen precu
26	149.5	14.8	435	2 I54182	tumor necrosis fac
27	143	14.2	277	2 I37552	OX40 homolog - hum
28	126	12.5	1790	1 MWFFB1	laminin beta-1 cha
29	122	12.1	305	2 A46476	B cell-associated

## RESULT 1

### GQMST1

tumor necrosis factor receptor 1 precursor - mouse

N;Alternate names: tumor necrosis factor receptor, 55K

C;Species: Mus musculus (house mouse)

C;Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004

C;Accession: A38634; B40254; S16677; S19021; I54532; I57826

R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E.

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A;Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor r

A;Reference number: A38634; MUID:91187885; PMID:1849278

A;Accession: A38634

A;Molecule type: mRNA

A;Residues: 1-454 <LEU>

A;Cross-references: UNIPROT:P25118; GB:M60468; NID:G199825; PIDN:AAA39751.1; PID:G199826

R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenk

Mol. Cell. Biol. 11, 3020-3026, 1991

A;Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A;Reference number: A40254; MUID:91246168; PMID:1645445

A;Accession: B40254

A;Molecule type: mRNA

A;Residues: 1-454 <GO2>

A;Cross-references: GB:M60468; NID:G199825; PIDN:AAA39751.1; PID:G199826

R;Barrett, K.; Taylor-Fishwick, D.A.; Cope, A.P.; Kissenerghis, A.M.; Gray, P.W.; Feldma

Eur. J. Immunol. 21, 1649-1656, 1991

A;Title: Cloning, expression and cross-linking analysis of the murine p55 tumor necrosis

A;Reference number: S16677; MUID:91285014; PMID:1647956

A;Accession: S16677

A;Molecule type: mRNA

A;Residues: 1-454 <BAR>

A;Cross-references: EMBL:X59238; NID:G53578; PIDN:CAA41922.1; PID:G53579

R;Rothe, J.G.; Brockhaus, M.; Gentz, R.; Lesslauer, W.

Immunogenetics 34, 338-340, 1991

A;Title: Molecular cloning and expression of the mouse Tnf receptor type b.

A;Reference number: S19021; MUID:92039815; PMID:1657766

A;Accession: S19021

A;Molecule type: mRNA

A;Residues: 1-454 <ROT>

A;Cross-references: EMBL:X57796; NID:G54848; PIDN:CAA40936.1; PID:G54849

R;Bebo, B.F.

Immunogenetics 39, 450-451, 1994

A;Title: Nucleotide sequence of the TNF type I receptor from a mouse endothelioma cell 1

A;Reference number: I54532; MUID:94245292; PMID:8188324

A;Accession: I54532

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-454 <RES>

A;Cross-references: GB:I26349; NID:G430732; PIDN:AAA59361.1; PID:G430733

R;Rothe, J.G.; Bluethmann, H.; Gentz, R.; Lesslauer, W.; Steinmetz, M.

Mol. Immunol. 30, 165-176, 1993

A;Title: Genomic organization and promoter function of the murine tumor necrosis factor

A;Reference number: I57826; MUID:93156721; PMID:8381516

membrane glycoprot  
lymphocyte activat  
laminin alpha 5 ch  
perlecan precursor  
major surface-labe  
T-cell antigen 4-1  
variant-specific s  
laminin B2t chain  
epidermal growth f  
hypothetical prote  
trophozoite surfac  
laminin gamma-1 ch  
heparan sulfate pr  
laminin beta-2 cha  
serine proteinase  
laminin gamma 2 ch

## ALIGNMENTS



**Qy** 21 LLLLLLLLLLNL-----PLQVKFAMLEHLSFKCPAGEY---WSKDVCCKNCAGTFVKA 71  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dd** 11 LSLVLLALLMGIIHPSGVTGLVPSLGDRKRDNLCPQGKYAHPKNNSICCTKCHKGYLVLS 70  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Qy** 72 PCRIPTQGOCEKCHPGTTEKDNLYLDACILSTCDKD--QEWVADCSATSDRKCOCRTG 129  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dd** 71 DCFSPQGETVCEYCDGTFTASQHNVRQLSCKTKEMFQVEISPCAKMDMTVCCKKN 130  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Qy** 130 LYI-YDPKPESPCTKTCPQGIPLVLQGNSTANTVCS 166  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dd** 131 QFORYLSETHFOVDGSCPFNG-TVTIPCKEKNTVCN 167  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
  
RESULT 3  
T28623  
hypothetical protein G2R - variola major virus  
C/Species: variola major virus  
C/Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 09-Jul-2004  
C/Acession: T28623  
R/Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Au  
Nature 366, 748-751, 1993  
A>Title: Potential virulence determinants in terminal regions of variola smallpox vir  
A/Reference number: Z20488; MUID:94088747; PMID:8264798  
A/Accession: T28623  
A/Status: preliminary;  
A/Molecule type: DNA  
A/Residues: 1-348 <WAS>  
A/Cross-references: UNIPROT:P34015; EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g4  
A/Experimental source: strain Bangladesh 1975  
C/Superfamily: TNF-alpha receptor-II, vaccinia C22L type; NGF receptor repeat homolog  
  
Query Match 20.0%; Score 201.5; DB 2; Length 348;  
Best Local Similarity 35.5%; Pred.No.3.4e-08;  
Matches 44; Conservative 18; Mismatches 55; Indels 7; Gaps 5;  
  
**Qy** 47 KCPAGBYWKDVCKNCAGTFVKAPCEIPHQTGGQCEKCHPGTTEKDNLYDACILCS-T 105  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dd** 30 KKCDTEYKRHHLCCLSCPPTVASRLCD-SKITNTQCTPCGSGTGFTSRNNHLPACLSCNGR 88  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Qy** 106 CDKQDQEWADCSATSDRKCQCRTGLYYDPKFPESCRPC---TKCPQGIPLVLQECNSTAN 162  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dd** 89 CNSNQVETRSCNTNHRI CECSFG-YCYLLKGSSGCKACVSQTKCGIGYGVSQH-TSVGD 146  
| | | | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Qy** 163 TVCS 166  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
**Dd** 147 VICS 150  
| | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :  
  
RESULT 4  
D36858  
Gene GAR protein - variola virus  
N/Alternate names: B28R protein (COP)  
C/Species: variola virus  
C/Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
C/Acession: D36858; S46888; S32385; S35987  
R/Blinov, V.M.  
submitted to GenBank, November 1992  
A/Reference number: A36859  
A/Accession: D36858  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-349 <BLI>  
A/Cross-references: UNIPROT:P34015; GB:X69198; NID:g456758; PIDN:CAA49137.1; PID:g457  
A/Experimental source: strain India-1967, ssp. major, isolate ind3  
R/Kolykhalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chizhikov, V.E.; F  
submitted to the EMBL Data Library, April 1992  
A/Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H  
A/Reference number: S46868  
A/Accession: S46888  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-349 <ROL>  
A/Cross-references: EMBL:X67117; NID:g516428; PIDN:CAA47540.1; PID:g516449

[illegible]

tumor necrosis factor receptor 1 precursor [validated] - human

N:Alternate names: p55 tumor necrosis factor receptor; TNF receptor type 1

N:Contains: tumor necrosis factor alpha inhibitor; tumor necrosis factor binding protein

C:Species: Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 09-Jul-2004

C:Accession: A32808; A34899; A34900; A36555; C36555; A36281; S12057; J07058; A60231; A38:A:Fuchs, P.; Strehl, S.; Dworzak, M.; Himmeler, A.; Ambros, P.F. Genomics 13, 219-224, 1992

A:Title: Structure of the human TNF receptor 1 (p60) gene (TNFRF1) and localization to chi

A:Reference number: A32808; UID:92250049; PMID:1315717

A:Accession: A32808

A:Molecule type: DNA

A:Residues: 1-455 <FUC>

A:Cross-references: UNIPROT:P19438; GB:M75864; GB:M75865; NID:G339748; PIDN:AJ

A:Loetscher, H.; Pan, Y.C.E.; Lahm, H.W.; Gentz, R.; Brockhaus, M.; Tabuchi, H.; Lesslaue

Cell 61, 351-359, 1990

A:Title: Molecular cloning and expression of the human 55 kd tumor necrosis factor recept

A:Reference number: A34899; UID:90235284; PMID:2158862

A:Accession: A34899

A:Molecule type: mRNA

A:Residues: 1-455 <LOB>

A:Cross-references: GB:M58286; GB:M33480; NID:G339753; PIDN:AAA36753.1; PID:G339754

A:Experimental source: Placenta

A:Note: part of this sequence, including the amino end of the mature protein, confirmed 1

R:Schall, T.J.; Lewis, M.; Koller, K.J.; Lee, A.; Rice, G.C.; Wong, G.H.W.; Gatanaga, T.

Cell 61, 361-370, 1990

A:Title: Molecular cloning and expression of a receptor for human tumor necrosis factor.

A:Reference number: A34900; UID:90235285; PMID:2158863

A:Accession: A34900

A:Molecule type: mRNA

A:Residues: 1-455 <SCH>

A:Cross-references: GB:M33294; NID:G339744; PIDN:AAA03210.1; PID:G339745

R:Himmeler, A.; Maurer-Fogy, I.; Kroenke, M.; Scheurich, P.; Pfizenmaier, K.; Lantz, M.; (

DNA Cell Biol. 9, 705-715, 1990

A:Title: Molecular cloning and expression of human and rat tumor necrosis factor recepto

A:Reference number: A36555; UID:91090841; PMID:1702293

A:Accession: A36555

A:Molecule type: mRNA

A:Residues: 1-455 <HIM>

A:Cross-references: GB:M63121; NID:G339755; PIDN:AAA36754.1; PID:G339756

A:Accession: A36555

A:Molecule type: protein

A:Residues: 30-38141-53, X', 55-79, 'XX', 82-94, 'NK', 'XX', 100-104, 107-128; 162-167, 'X', 169-21

A:Note: the purified protein, called tumor necrosis factor binding protein, is a soluble

R:Gray, P.W.; Barrett, K.; Chantry, D.; Turner, M.; Feldmann, M.

Proc. Natl. Acad. Sci. U.S.A. 87, 7380-7384, 1990

A:Title: Cloning of human tumor necrosis factor (TNF) receptor cDNA and expression of re

A:Reference number: A3281; UID:91017509; PMID:2170974

A:Accession: A3281

A:Molecule type: mRNA

A:Residues: 1-455 <GRA>

A:Cross-references: GB:M37764

A:Note: the authors translated the codon TGG for residue 371 as Thr, AAG for residue 372

R:Nophar, Y.; Kemper, O.; Brakebusch, C.; Engelmann, H.; Zwang, R.; Aderka, D.; Holtmann

EMBO J. 9, 3269-3278, 1990

A:Title: Soluble forms of tumor necrosis factor receptors (TNF-Rs). The cDNA for the typ

le form of the receptor.

A:Reference number: S12057; UID:91006021; PMID:1698610

A:Accession: S12057

A:Molecule type: mRNA

A:Residues: 1-455 <NOP>

A:Cross-references: ENBL:X55313; NID:G37223; PIDN:CAA39021.1; PID:G37224

A:Note: parts of soluble TNF binding protein 1, including its amino and carboxyl ends, w

R:Kemper, O.; Wallach, D.

Gene 134, 209-216, 1993

A:Title: Cloning and partial characterization of the promoter for the human p55 tumor ne

A:Reference number: J07058; UID:94085779; PMID:8262379

A:Accession: J07058

A:Molecule type: DNA

A:Residues: 1-13 <KEM>

R:Seckinger, P.; Vey, E.; Turcatti, G.; Wingfield, P.; Dayer, J.M.

Eur. J. Immunol. 20, 1167-1174, 1990

A:Title: Tumor necrosis factor inhibitor: purification, NH-2-terminal amino acid sequenc

A:Reference number: A60231; MUID:90292116; PMID:2113477  
 A:Accession: A60231  
 A:Molecule type: protein  
 A:Residues: 41-43,'X',45-53,'X',55-57 <SCS>  
 R:Gatanaga, T.; Hwang, C.; Kohr, W.; Cappuccini, F.; Lucci III, J.A.; Jeffes, E.W.B.; Le Proc. Natl. Acad. Sci. U.S.A. 87, 8781-8784, 1990  
 A:Title: Purification and characterization of an inhibitor (soluble tumor necrosis factor) of tumor necrosis factor.  
 A:Reference number: A38258; MUID:91062364; PMID:2174164  
 A:Accession: A38258  
 A:Molecule type: protein  
 A:Residues: 41-60 <GAT>  
 A:Experimental source: cancer patient serum  
 R:Olsson, I.; Lantz, M.; Nilsson, E.; Petre, C.; Thysell, H.; Grubb, A.; Adolf, G. Eur. J. Haematol. 42, 270-275, 1989  
 A:Title: Isolation and characterization of a tumor necrosis factor binding protein from human urine.  
 A:Reference number: A60594; MUID:89171156; PMID:2924890  
 A:Accession: A60594  
 A:Molecule type: protein  
 A:Residues: 41-43,'X',45-53,'V',55-57,'XK',60 <OLS>  
 A:Experimental source: renal failure patient urine  
 R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990  
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence for two distinct binding sites.  
 A:Reference number: A35010; MUID:90110215; PMID:2153136  
 A:Accession: A35010  
 A:Molecule type: protein  
 A:Residues: 41-45 <ENG>  
 A:Experimental source: normal urine  
 R:Kajihara, J.; Asada, A.; Kirihara, S.; Kato, K. Biochem. Biotechnol. Biochem. 58, 2266-2268, 1994  
 A:Title: Amino acid sequence of natural tumor necrosis factor alpha inhibitor purified from human urine.  
 A:Reference number: JC2404; MUID:95128033; PMID:7765720  
 A:Accession: JC2404  
 A:Molecule type: protein  
 A:Residues: 41-53,'X',55-144,'X',146-150,'X',152-186,'X',188-201 <KAJ>  
 A:Experimental source: urine  
 C:Comment: This protein is one of two known receptors for both TNF-alpha (cachectin) and TNF-beta (lymphotoxin).  
 A:Gene: TNFR1  
 A:Cross-references: GDB:125913; OMIM:191190  
 A:Map position: 12p13.2-12p13.2  
 A:Introns: 13/3; 65/1; 108/1; 158/1; 184/2; 209/1; 247/1; 256/3; 353/1  
 C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homologous to TNF receptor; glycoprotein; receptor; transmembrane protein  
 F:1-21/Domain: signal sequence #status predicted <SIG>  
 F:22-45/Domain: signal sequence #status predicted <SIG>  
 F:46-201/Domain: extracellular #status predicted <EXT>  
 F:202-211/Domain: transmembrane #status predicted <TM>  
 F:212-234/Domain: transmembrane #status predicted <TM>  
 F:235-455/Domain: intracellular #status predicted <INT>  
 F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 20.0%; Score 201.5; DB 1; Length 455;  
 Best Local Similarity 30.6%; Pred. No. 4.1e-08;  
 Matches 49; Conservative 21; Mismatches 73; Indels 17; Gaps 5;  
 Qy 23 LLLLLLLLLPLQV-----KFMLELHSPKCPAGEY---WSKDVCKNCSAGTFV 69  
 Db LLLPLVLELVAVGTPSGVGLVPLHGLDREKRDVCPQGYIHPQNNISCTCKCHKGYL 68  
 Qy 70 KAPEIPTHQCCQCKHPGFTEDKNDYLDACILCTCDK--QEMVADCSATSDRKCCQR 127  
 Db YNDCPGFGQDTDCRECSGSGFTASENHLRCLSCSKCKEMQGVETSSCTVDRDVTVCGR 128  
 Qy 128 TGLY--YDPRFPESCRCPTCKPQGPVLOECNSTANTVCS 166  
 Db LKQYRHYWSENLFCQFNCSLCLNG--TVHLSQEQKQNTVCT 167

## RESULT 7

JC4302  
 tumor necrosis factor receptor p55 precursor - pig  
 C:Species: Sus scrofa domestica (domestic pig)  
 C:Date: 29-Nov-1995 #sequence\_revision 08-Feb-1996 #text\_change 09-Jul-2004  
 C:Accession: JC4302; PC4093  
 R:Suter, B.; Pauli, U.  
 Gene 163, 263-266, 1995  
 A:Title: Cloning of the cDNA encoding the porcine p55 tumor necrosis factor receptor.  
 A:Reference number: JC4302; MUID:96011645; PMID:7590278  
 A:Accession: JC4302  
 A:Molecule type: mRNA  
 A:Residues: 1-461 <SUT>  
 A:Cross-references: UNIPROT:P50555; GB:U19994; NID:gl141752; PIDN:AAC48499.1; PID:gl141752  
 A:Accession: PC4093  
 A:Molecule type: protein  
 A:Residues: 1-7 <SU2>  
 A:Experimental source: kidney cell line 15  
 C:Genetics:  
 C:Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homologous to TNF receptor; glycoprotein; kidney; receptor; transmembrane protein; tumor

F:1-29/Domain: signal sequence #status predicted <SIG>  
 F:30-461/Product: tumor necrosis factor receptor p55 #status predicted <MAT>  
 F:44-194/Domain: extracellular cysteine rich #status predicted <EXT>  
 F:84-82/Domain: NGF receptor repeat homology <NG1>  
 F:84-126/Domain: NGF receptor repeat homology <NGF>  
 F:211-231/Domain: transmembrane #status predicted <TM>  
 F:361-447/Domain: signal transduction #status predicted <SIT>  
 F:54,145,151/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 Query Match 19.9%; Score 200.5; DB 2; Length 461;  
 Best Local Similarity 30.8%; Pred. No. 4.9e-08;  
 Matches 49; Conservative 25; Mismatches 70; Indels 15; Gaps 7;  
 Qy 21 LLLLLLLLLLNL-PLQVFMFL-----ELHSFKCPAGEY---WSKDVCKNCSAGTFVKA 71  
 Db LLLPLVLELVAVGTPSGVGLVPLHGLDREKRDVCPQGYIHPQNNISCTCKCHKGYLHN 70  
 Qy 72 PCEIPHTQGOCEKCHPCTETEDKNDYLDACILCTC--DKQEMVADCSATSDRKCCQRTG 129  
 Db DCLGPGGLDTCRECDNGTFTASENHLTQCLSCSKCKEMQGVETSSCTVDRDVTVCGRKN 130  
 Qy 130 LY--YDPRFPESCRCPTCKPQGPVLOECNSTANTVCS 166  
 Db LKQYRHYWSENLFCQFNCSLCLNG--TVHLSQEQKQNTVCT 167

## RESULT 8

SI2783  
 OX40 antigen precursor - rat  
 N:Alternate names: nerve growth factor receptor homolog  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 09-Jul-2004  
 C:Accession: SI2783; S08036  
 R:Mallett, S.; Fosssum, S.; Barclay, A.N.  
 EMBO J. 9, 1063-1068, 1990  
 A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes.  
 A:Reference number: SI2783; MUID:90214614; PMID:2157591  
 A:Accession: SI2783  
 A:Molecule type: mRNA  
 A:Residues: 1-271 <MAL>  
 A:Cross-references: UNIPROT:P15725; EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:g57830  
 C:Superfamily: CD27 antigen; NGF receptor repeat homologous to TNF receptor; glycoprotein; transmembrane protein  
 F:1-19/Domain: signal sequence #status predicted <SIG>  
 F:20-271/Product: OX40 antigen #status predicted <MAT>  
 F:212-235/Domain: transmembrane #status predicted <TM>

Query Match 18.7%; Score 188; DB 2; Length 271;  
 Best Local Similarity 27.1%; Pred. No. 2.9e-07;  
 Matches 51; Conservative 28; Mismatches 69; Indels 40; Gaps 9;  
 Qy 23 LLLLLLLLLPLQV-----KFMLELHSPKCPAGEY---WSKDVCKNCSAGTFV 69  
 Db LLLPLVLELVAVGTPSGVGLVPLHGLDREKRDVCPQGYIHPQNNISCTCKCHKGYL 68  
 Qy 70 KAPEIPTHQCCQCKHPGFTEDKNDYLDACILCTCDK--QEMVADCSATSDRKCCQR 127  
 Db YNDCPGFGQDTDCRECSGSGFTASENHLRCLSCSKCKEMQGVETSSCTVDRDVTVCGR 128  
 Qy 128 TGLY--YDPRFPESCRCPTCKPQGPVLOECNSTANTVCS 166  
 Db LKQYRHYWSENLFCQFNCSLCLNG--TVHLSQEQKQNTVCT 167

Cell 47, 545-554, 1986

A;Title: Expression and structure of the human NGF receptor.  
A;Reference number: A25218; MUID:87051725; PMID:3022937

A;Accession: A25218

A;Molecule type: mRNA

A;Residues: 1-427 <JOH>

A;Cross-references: UNIPROT:P09138; GB:M14764; NID:gl89204; PIDN:AAB59544.1; PID:gl89205

R;Marano, N.; Dietzschold, B.; Barley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.; J. Neurochem. 48, 225-232, 1987

A;Title: Purification and amino terminal sequencing of human melanoma nerve growth factor; A;Reference number: A60204; MUID:87085574; PMID:3025363

A;Accession: A60204

A;Molecule type: protein

A;Residues: 29-31, T', 33-42, TT', 45-46, TX', 50-51, 'XX', 54-56 <MAR>

A;Experimental source: melanoma cell line A875

R;Vissavajjhala, P.; Leszyk, J.D.; Lin-Goeke, J.; Ross, A.H. Arch. Biochem. Biophys. 294, 244-252, 1992

A;Title: Structural domains of the extracellular domain of human nerve growth factor receptor; A;Reference number: S21689; MUID:92198017; PMID:1372492

A;Accession: S21689

A;Status: preliminary

A;Molecule type: protein

A;Residues: 183-208 <VIS>

R;Sengal, A.; Patil, N.; Chao, M. Mol. Cell. Biol. 8, 3160-3167, 1988

A;Title: A constitutive promoter directs expression of the nerve growth factor receptor; A;Reference number: I57638; MUID:89096903; PMID:2850481

A;Accession: I57638

A;Status: preliminary; translated from GB/EMBL/DBDJB

A;Molecule type: DNA

A;Residues: 1-22 <RES>

A;Cross-references: GB:M21621; NID:gl89206; PIDN:AAA36363.1; PID:gl89207

C;Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma cells. The cytosine-rich region of the extracellular domain may form part or all of a binding site for the nerve growth factor.

C;Comment: This protein is thought to form a high-affinity receptor when it associates with nerve growth factor.

C;Comment: This receptor undergoes both N- and O-linked glycosylation.

C;Genetics:

A;Gene: GDB:NGFR

A;Cross-references: GDB:I20234; OMIM:162010

A;Map position: 17q21-17q22

C;Superfamily: nerve growth factor receptor; NGF receptor repeat homology

C;Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t

F;1-28/Domain: signal sequence #status predicted <SIG>

F;29-427/Product: nerve growth factor receptor #status experimental <MAT>

F;29-250/Domain: extracellular #status predicted <EXT>

F;32-65/Domain: NGF receptor repeat homology <NG1>

F;67-108/Domain: NGF receptor repeat homology <NG2>

F;109-147/Domain: NGF receptor repeat homology <NG3>

F;149-189/Domain: NGF receptor repeat homology <NG4>

F;197-248/Region: serine/threonine-rich

F;251-272/Domain: transmembrane #status predicted <INT>

F;273-427/Domain: intracellular #status predicted <INT>

F;60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 18.7%; Score 188; DB 1; Length 427;  
Best Local Similarity 34.7%; Pred. No. 46-07;  
Matches 50; Conservative 11; Mismatches 69; Indels 14; Gaps 5;

Qy	24	LLLLLLLLLP- QVKFAMLEHSPKPAGEYWSKDVCKNCNSAGTVPKAPCEIPHTQGQC	82
Db	15	LLLLLLLLGVSLGGAKEA-----CPTGLYTHSGECKKACNLGEGVAQPCGA--NQTV	64
Qy	83	EKCHPG-TFTEKDNVLDACILCSTCKDQEMVADCSATSDRKCQCRGTGLYYDPKPPESC	141
Db	65	EPCLDSVTFSVDVSGATEPKCKTECVGLQSMAPCV EADDAVCRCAYG--YYQDETGR	122
Qy	142	RPCTKCPQGIPIVLOECNSTANTVC	165
Db	123	EACRVCEAGSLVTFSCQDKQNTVC	146

RESULT 11

Qy 116 CSATSRDKQCRTGLYYDPKPPESCRCPTCKPQGIPVLQECNSTANTVCSVSRR 172  
| : | : | : | : | : | : | : | : | : | : | : | : | :  
Db 119 CTRTONTKCRCKPN-FFCNSTVCEHCDPCCTCKEHGI--IKECTLTSNTKCKBEVRK 172

RESULT 13  
JC7705  
death receptor-6 - chicken  
C/Species: Gallus gallus (chicken)  
C/Date: 09-Nov-2001 #sequence\_revision  
C/Accession: JC7705  
R/Bridgham, J.T.; Bobe, J.; Goetz, F.W.; Johnson, A.L.  
Biochem. Biophys. Res. Commun. 284, 1103-1115, 2001  
A/Title: Conservation of death receptor-6 in avian and piscine vertebrates.  
A/Reference number: JC7705; MUID:21308433; PMID:11414698  
A/Accession: JC7705  
A/Molecule type: mRNA  
A/Residues: 1-651 <BRI>  
A/Cross-references: UNIPROT:Q98SW6; GB:AF349908  
C/Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs to the TNF superfamily. It is expressed in various tissues and/or survival signaling cascade.  
C/Genetics:  
A/Gene: dr-6  
C/Superfamily: tumor necrosis factor receptor type 1 (TNFR1); NGF receptor repeat homology domain  
C/Keywords: ovary  
F/1-21/Domain: signal sequence #status predicted <SIG>  
F/52-196/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>  
F/332-350/Domain: transmembrane #status predicted <TM>  
F/410-475/Domain: death domain #status predicted <DED>  
F/551-651/Region: conserved cytoplasmic #status predicted

Query Match 17.9%; Score 180.5; DB 2; Length 651;  
Best Local Similarity 29.8%; Pred. No. 1.9e-06;  
Matches 45; Conservative 27; Mismatches 66; Indels 13; Gaps 5;

Qy 22 LLLLLLLLNLPLQVKFAMLEHLHSFKCPAGEY-----WSKDVCCKNCAGTFVKAPCEI 75  
: | : | : | : | : | : | : | : | : | : | : | : | :  
Db 9 VLPLLVLFLGTADAQPKLTS-EQNASVSLPAGKYLHLDRATNQELICDCKPAGTYVSKHC-T 66  
: | : | : | : | : | : | : | : | : | : | : | : | :

Qy 76 PHTGOGCEKHCPCTTEFTKKNLYLDACILC-STCDKQEMVADCSATSDRKCOCRTGLYYVD 134  
: | : | : | : | : | : | : | : | : | : | : | : | :  
Db 67 KSTLRCSFCPDGTTFFKHENGIERCHPCPKPELPMIEKTHCTALTDRECTCLSGTF---- 123

Qy 135 KPFPESCRPCTKCPQIGIPVLQECNSTANTVC 165  
: | : | : | : | : | : | : | : | : | : | : | : | :  
Db 124 -GINDTCPVTYPCVGWGVKKGTETEDVRC 153  
: | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 14  
A40036 apoptosis-mediating surface antigen Fas precursor - human  
N;Alternate names: surface antigen APO-1  
C;Species: Homo sapiens (man)  
C;Date: 17-Jan-1992 #sequence\_revision 17-Jan-1992 #text\_change 09-Jul-2004  
C;Accession: A40036; S24543; A38142  
R;Itch, N.; Yonehara, S.; Ishii, A.; Yonehara, M.; Mizushima, M.; Hamaoka, H.  
Cell 66, 233-243, 1991  
A;Title: The polypeptide encoded by the cDNA for human cell surface antigen Fas can mediate apoptosis in T lymphocytes  
A;Reference number: A40036; MUID:91309137; PMID:1713127  
A;Accession: A40036  
A>Status: preliminary  
A:Molecule type: mRNA  
A;Residues: 1-335 <TO>  
A;Cross-references: UNIPROT:P25445; GB:M67454; NID:G182409; PIDN:AAA63174.1; PID:G182409  
R;Krammer, P.H.  
submitted to the EMBL Data Library, February 1992  
A;Reference number: S24543  
A;Accession: S24543  
A>Status: preliminary  
A:Molecule type: mRNA  
A;Residues: 1-335 <KRA>  
A;Cross-references: EMBL:X63717; NID:Q28741; PID:Q28742

```

F;141-181/Domain: NCF receptor repeat homology <NC4>
F;189-237/Region: serine/threonine-rich
F;240-361/Domain: transmembrane #status predicted <MEM>
F;262-416/Domain: intracellular #status predicted <INT>
F;52/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match      17.5%; Score 176.5; DB 1; Length 416;
Best Local Similarity 30.7%; Pred. No. 2.8e-06;
Matches 43; Conservative 20; Mismatches 68; Indels 9; Gaps 4;

Qy  27  LLALNLPLOVKFAMLELHSPKPAGEVSWKDVCKKNCAGTFVKAPCEIPIHTGQCEKCH 86
Db    7  LLLELLPAGTWSGKE---KCLTKMYTTSGBGCKACNLGEGVQVQPGV--NQTVCPCPL 60

Qy  87  PG-TFTEKDNLDACILCSCTCDKQEMVADCSATSDRKCOCRTGLYYDPKPFESCRPCT 145
Db    61  DSVYTSVTSGATPCKPCTQCVGLHMSAPCVESDDAVCRCAYG--YFQDELSGSCKECS 118

Qy  146  KCPQGIPVLQECNSTANTVC 165
Db    119  ICEVGFLMFPCCRDSDQTVTC 138

Search completed: September 9, 2005, 09:31:39
Job time : 131.476 secs

```

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: September 8, 2005, 23:31:32 ; Search time 672.857 Seconds  
(without alignments)  
136.989 Million cell updates/sec

Title: US-10-622-407-10

Perfect score: 1008

Sequence: 1 MFQFFCSLVSLRFLMRR.....ANTVCSSVSRRSASVAVPI 180

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

UniProt\_03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	956	94.8	198	1 TR22 MOUSE	Q9er62 mus musculus
2	705	69.9	176	1 TR23 MOUSE	Q9er63 mus musculus
3	299	29.7	204	1 TR26 MOUSE	P83626 mus musculus
4	286.5	28.4	225	2 Q7T3M7	Q7t3m7 gallus gall
5	286.5	28.4	410	2 Q7T3M8	Q7t3m8 gallus gall
6	275.5	27.3	438	2 Q9DFV0	Q9dfv0 brachydanio
7	273.5	27.1	395	2 Q800K8	Q800k8 paralichthy
8	259	25.7	357	2 Q9DF34	Q9df34 brachydanio
9	249.5	24.8	321	2 Q6DJ81	Q6dj81 xenopus tro
10	249	24.7	328	2 Q76B99	Q76b99 xenopus lae
11	248	24.6	328	2 Q6GLZ4	Q6glz4 xenopus lae
12	239.5	23.8	289	2 Q678B7	Q678b7 lymphocysti
13	239	23.7	189	2 Q95N85	Q95n85 felis silve
14	233	23.1	446	2 Q95ND3	Q95nd3 felis silve
15	232	23.0	328	2 Q76B98	Q76b98 xenopus lae
16	221	21.9	347	2 Q57119	Q57119 cowpox viru
17	217.5	21.6	440	2 Q6QHF2	Q6qhf2 mus musculus
18	217.5	21.6	440	2 Q6QHF1	Q6qhf1 mus musculus
19	217.5	21.6	454	1 TR1A MOUSE	P25118 mus musculus
20	216	21.4	189	2 Q97530	Q97530 canis famil
21	216	21.4	360	2 Q57118	Q57118 cowpox viru
22	215.5	21.4	326	2 Q57120	Q57120 cowpox viru
23	215.5	21.4	348	2 Q57103	Q57103 monkeypox v
24	215.5	21.4	348	2 Q57108	Q57108 monkeypox v
25	215.5	21.4	348	2 Q57277	Q57277 monkeypox v
26	215.5	21.4	349	2 Q57271	Q57271 monkeypox v
27	215.5	21.4	349	2 Q57102	Q57102 monkeypox v
28	215.5	21.4	349	2 Q57291	Q57291 monkeypox v
29	215.5	21.4	349	2 Q57305	Q57305 cowpox viru
30	215.5	21.4	351	2 Q57121	Q57121 cowpox viru
31	215	21.3	323	1 TNR6_BOVIN	P51867 bos taurus

## RESULT 1

ID	TR22_MOUSE	STANDARD;	PRT;	198 AA.
AC	Q9ER62: Q8VHB9; Q9CZA4;			
DT	28-FEB-2003 (Rel. 41, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DE	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 22 (Tumor necrosis factor receptor p60 homolog 2) (TNF receptor family member SOBA)			
DE	(Decoy TRAIL receptor 2) (TNF receptor homolog 2)			
GN	Names=fnfr1f22; Synonyms=DcTrailr2, Tnfrh2, Tnfrsf1a2;			
OS	Mus musculus (Mouse)			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	STRAIN=129/SV; TISSUE=Embryonic stem cells;			
RX	MEDLINE=20519229; PubMed=11063728; DOI=10.1093/hmg/9.18.2691;			
RA	Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,			
RA	Lane N., Reik W., Walter J.,			
RT	"Sequence and functional comparison in the Beckwith-Wiedemann region; implications for a novel imprinting centre and extended imprinting."			
RL	Hum. Mol. Genet. 9:2691-2706(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), FUNCTION, AND 3D-STRUCTURE			
RC	MODELING OF 62-170.			
RX	STRAIN=NIH Swiss;			
RA	PubMed=12466268; DOI=10.1074/jbc.M210783200;			
RA	Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A.,			
RA	Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,			
RA	Burkly L.C., Techoop J., Zheng T.S.,			
RT	"Identification of a new murine tumor necrosis factor receptor locus that contains two novel murine tumor necrosis factor receptor factor-related apoptosis-inducing ligand (TRAIL).";			
RL	J. Biol. Chem. 278:5444-5454(2003).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RA	Risser P., Mao W., Baldwin D.T., Pan G.,			
RT	"Characterization of SOBA, a murine member of the TNFR family."			
RL	Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A. (ISOFORM 2).			
RC	STRAIN=C57BL/6J; TISSUE=Embryo;			
RX	MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;			
RA	Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,			
RA	Nikazaki I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,			
RA	Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schorbach C., Gojobori T.,			
RA	Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,			
RA	Schriml L.M., Kanapin A., Matusda H., Batalov S., Beisel K.W.,			
RA	Blake J.A., Bradt D., Brusica V., Chothia C., Corbani L.E., Cousins S.,			
RA	Dalla E., Dragani T.A., Fletcher C.F., Forrester A., Frazer K.S.,			
RA	Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,			
RA	Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,			

## ALIGNMENTS

32	214.5	21.3	440	2	Q6QHF2
33	213.5	21.2	253	2	Q6WB14
34	213.5	21.2	326	2	O57122
35	213.5	21.2	351	1	CRMB COMPX
36	212.5	21.1	349	2	O57099
37	211.5	21.0	318	2	Q7T2H3
38	211.5	21.0	332	1	TNR6_PIG
39	211	20.9	263	2	Q9XS60
40	211	20.9	320	2	Q9TV79
41	211	20.9	319	2	Q9XS29
42	210.5	20.9	347	2	O57115
43	209.5	20.8	349	1	CRMB CAMPS
44	209.5	20.8	349	2	O57098
45	209.5	20.8	349	2	O57100

Q6qhf2	mus	spretus
Q6wb14	callithrix	
O57122	cowpox viru	
O73559	cowpox viru	
O57099	monkeypox v	
Q7t2h3	oncorhynch	
O7736	sus scrofa	
Q9xs60	oryctolagus	
Q9tv79	oryctolagus	
Q9xs29	oryctolagus	
O57115	cowpox viru	
O8uva7	camelopard	
O57098	camelopard	
O57100	monkeypox v	

FT	REPEAT	84	124	TNFR-Cys 2.
FT	REPEAT	125	165	TNFR-Cys 3.
FT	DISULFID	48	59	By similarity.
FT	DISULFID	60	73	By similarity.
FT	DISULFID	63	82	By similarity.
FT	DISULFID	85	100	By similarity.
FT	DISULFID	103	116	By similarity.
FT	DISULFID	106	124	By similarity.
FT	DISULFID	126	141	By similarity.
FT	DISULFID	144	157	By similarity.
FT	DISULFID	147	165	By similarity.
FT	CARBOHYD	62	62	N-linked (GlcNAc. .) (Potential).
FT	CARBOHYD	158	158	N-linked (GlcNAc. .) (Potential).
FT	VARSPLIC	171	198	NPRLRFLLSPLSLVSVLVVFRIIR -> RRSASVAMP I (in isoform 2). /FTId=VSP_007648. L -> V (in Ref. 2). L -> C (in Ref. 1); CAC16406). LLLL -> CVV (in Ref. 1; CAC16406).
SQ	SEQUENCE	198 AA;	22375 MW;	EBF8F52961EA9983 CRC64;
Query Match		94.8%;	Score 956;	DB 1; Length 198;
Best Local Similarity		100.0%;	Pred. No. 5.3e-75;	
Matches 170;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
QY	1	MFGFFCSLVSSLSRWFLWRRLRLLLLLLNLPLQVKFAMLEHSHFKPAGEWSKDVCC	60	
DB	1	MFGFFCSLVSSLSRWFLWRRLRLLLLLLNLPLQVKFAMLEHSHFKPAGEWSKDVCC	60	
QY	61	KNCAGTFVKAPCEIPHTTGOGEKCHPGFTTEKDNYLDACILCSTCKDQDMVADCSATS	120	
DB	61	KNCAGTFVKAPCEIPHTTGOGEKCHPGFTTEKDNYLDACILCSTCKDQDMVADCSATS	120	
QY	121	DRKCQRTGLYYDDPKFPESCRCPTKCPQGIPVLQECNSTANTVCSSSVS	170	
DB	121	DRKCQRTGLYYDDPKFPESCRCPTKCPQGIPVLQECNSTANTVCSSSVS	170	
RESULT 2				
TR23 MOUSE		STANDARD;	PRT;	176 AA.
ID	TR23_MOUSE			
AC	Q9ER63; Q8VHC0;			
CD	28-FEB-2003 (Rel. 41, Created)			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DE	05-JUL-2004 (Rel. 44, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 23 precursor (Tumor			
DE	necrosis factor receptor p60 homolog 1) (TNF receptor family member			
DE	SOB) (Decoy TRAIL receptor 1) (TNF receptor homolog 1).			
GN	Names=Tnf1st23; Synonyms=Dctrailr1, Tnfrh1, Tnfrsf11;			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_Taxid=10090;			
RX	[1]			
RC	SEQUENCE FROM N.A.			
RC	STRAIN=129/Sv; TISSUE=Embryonic stem cells;			
RX	MEDLINE=20519229; PubMed=11063728; DOI=10.1093/bmg/9.18.2691;			
RA	Engemann S., Stroedicke M., Paulsen M., Franck O., Reinhardt R.,			
RA	Lane N., Reik W., Walter J.;			
RT	"Sequence and functional comparison in the Beckwith-Wiedemann region:			
RT	implications for a novel imprinting centre and extended imprinting.";			
RL	Hum. Mol. Genet. 9:2691-2706(2000).			
RP	[2].			
RP	SEQUENCE FROM N.A.; FUNCTION, SUBCELLULAR LOCATION, AND 3D-STRUCTURE			
RP	MODELING OF 52-160.			
RC	STRAIN=C57BL/6;			
RX	PubMed=12466268; DOI=10.1074/jbc.M210783200;			
RA	Schneider P., Olson D., Tardivel A., Browning B., Lugovsky A.,			
RA	Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,			
RA	Burkly L.C., Tschopp J., Zheng T.S.;			
RT	"Identification of a new murine tumor necrosis factor receptor locus			
RT	that contains two novel murine receptors for tumor necrosis factor-			
RT	related apoptosis-inducing ligand (TRAIL).";			

J. Biol. Chem. 278:5444-5454 (2003).

[3] SEQUENCE FROM N.A.

RT Pan G., Mao W., Rissler P.;

RT "Characterization of SOB, a member of the TNFR family.";

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: Receptor for the cytotoxic ligand TRAIL. Lacks a

CC cytoplasmic death domain and hence is not capable of inducing

CC apoptosis. May protect cells against TRAIL mediated apoptosis

CC through ligand competition. Cannot induce the NF-kappa-B pathway.

CC -1- SUBCELLULAR LOCATION: Ubiquitous.

CC -1- TISSUE SPECIFICITY: Ubiquitous.

CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC or send an email to license@isb-sib.ch).

CC -----

DR ENBL; AJ278264; CAC16405.1; -.

DR ENBL; AJ276505; CAC27352.1; -.

DR ENBL; AY165825; AAN87805.1; -.

DR ENBL; AY046550; AAL05072.1; -.

DR HSSP; Q92956; IJMA.

DR MGD; MGI:1930269; Tnfrsf23.

DR GO; GO:0005515; F:protein binding; IPI.

DR GO; GO:0005031; F:tumor necrosis factor receptor activity; IDA.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 3.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR NGFR\_1; 3.

DR PROSITE; PS00050; TNFR NGFR\_2; 2.

KW Glycoprotein; GPI-anchor; Lipoprotein; Receptor; Repeat; Signal.

FT SIGNAL 1 29

FT CHAIN 30 155 Tumor necrosis factor receptor

FT superfamily member 23.

FT PROPEP 156 176 Removed in mature form (Potential).

FT LPID 155 155 GPI-anchor amidated cysteine (Potential).

FT REPEAT 37 72 TNFR-Cys 1.

FT REPEAT 74 114 TNFR-Cys 2.

FT REPEAT 115 155 TNFR-Cys 3.

FT DISULFID 38 49 By similarity.

FT DISULFID 50 63 By similarity.

FT DISULFID 53 72 By similarity.

FT DISULFID 75 90 By similarity.

FT DISULFID 93 106 By similarity.

FT DISULFID 96 114 By similarity.

FT DISULFID 116 131 By similarity.

FT DISULFID 134 147 By similarity.

FT DISULFID 137 155 By similarity.

FT CARBOHYD 148 148 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 176 AA; 19594 MW; BE30D617F49DDB7D CRC64;

Query Match 69.9%; Score 705; DB 1; Length 176;

Best Local Similarity 79.9%; Pred. No. 2.5e-53;

Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY 7 SLVSSLSRWFLMRLRLLLLLLLNLPLQVKFAMLELHSPKCPAGEYWSKDVCKKCSAG 66

DB 5 SHVSSLSLHWF-----LLLLLLNLPLPFIAMPESYFNCPCDGEYQSDVCKTCPSG 56

QY 67 TFVKAPCEIHTGOCCKCHPGFTTEKDYNLDCILCSTCDKQDMVADCSATSDRKCC 126

DB 57 TFVKAPCKIHTGQCKCHPGFTTGKNDGLHDCILCSTCDKQDMVADCSATSDRKCEC 116

QY 127 RTGLYYDDPKFPSPSCRCCTKCPQIGPVLQCNSTANTVCSSSVS 170

DB 117 QIGLYYDDPKFPSPSCRCCTKCPQIGPVLQCNSTANTVCSSSVS 160

RESULT 3

TR26 MOUSE STANDARD; PRT; 204 AA.

ID TR26\_MOUSE

AC P83626;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 26 precursor (TNF

DE receptor homolog 3).

GN Names:Tnfrsf26; Synonyms=Tnfrh3;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND 3D-STRUCTURE MODELING OF

RP 41-148.

RC STRAIN=C57BL/6; TISSUE=Spleen;

RX PubMed=12466268; DOI=10.1074/jbc.M210783200;

RA Schneider P., Olson D., Tardivel A., Browning B., Lugovskoy A., Hsu Y.-M.,

RA Gong D., Dobles M., Hertig S., Hofmann K., Van Vlijmen H., Hsu Y.-M.,

RA Burkly L.C., Teichopp J., Zheng T.S.;

RT "Identification of a new murine tumor necrosis factor receptor locus

RT that contains two novel murine receptors for tumor necrosis factor-

RT related apoptosis-inducing ligand (TRAIL).";

RL J. Biol. Chem. 278:5444-5454 (2003).

CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: Expressed in thymus and spleen. Detectable

CC levels in lung.

CC -1- SIMILARITY: Contains 3 TNFR-Cys repeats.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AY165628; AAN87808.1; -.

DR MGD; MGI:2651928; Tnfrsf26.

DR InterPro; IPR001368; TNFR\_c6.

DR Pfam; PF00020; TNFR\_c6; 3.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR NGFR\_1; 3.

DR PROSITE; PS00050; TNFR NGFR\_2; 2.

KW Glycoprotein; Receptor; Repeat; Signal; Transmembrane.

FT SIGNAL 1 19 Potential.

FT CHAIN 20 204 Tumor necrosis factor receptor

FT superfamily member 26.

FT DOMAIN 20 164 Extracellular (Potential).

FT TRANSMEM 165 185 Potential.

FT DOMAIN 186 204 Cytoplasmic (Potential).

FT REPEAT 27 61 TNFR-Cys 1.

FT REPEAT 63 103 TNFR-Cys 2.

FT REPEAT 104 143 TNFR-Cys 3.

FT DOMAIN 38 126 Cys-rich.

FT DISULFID 27 38 By similarity.

FT DISULFID 39 52 By similarity.

FT DISULFID 42 61 By similarity.

FT DISULFID 64 79 By similarity.

FT DISULFID 82 95 By similarity.

FT DISULFID 85 103 By similarity.

FT DISULFID 105 120 By similarity.

FT DISULFID 123 135 By similarity.

FT DISULFID 126 143 By similarity.

FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).

FT CARBOHYD 136 136 N-linked (GlcNAc...) (Potential).

SQ SEQUENCE 204 AA; 22708 MW; A35C5177F178C3DD CRC64;

Query Match 29.7%; Score 299; DB 1; Length 204;

Best Local Similarity 41.3%; Pred. No. 3.8e-18;

Matches 59; Conservative 24; Mismatches 56; Indels 4; Gaps 3;

```

Qy 24 LLLLLLLNLPQVKFAMLELHSPK-CPAGEYWSKDVCKKNSAGTFVKAPCEIPHTQGC 82
Db 4 LRLLLLLGLLRV--AVCSNITFLCKIGFPHKHNLCCLQCSAGTYLRNQCQENHNKSEC 61
Qy 83 EKCHPGFTTEKDNVLDACILSTCDKQEMVADCSATSDRKCQCRTGLYYYPKPSR 142
Db 62 APCDSEHFIDHNKRESGFCPSVCRDQEEVAKSRADRVCCQKQGTGTCDSNCLERCH 121
Qy 143 PCTKCPQGPVLOECNSTANTVC 165
Db 122 TCSSCPDG-RVVRKCNATMDTVC 143

RESULT 4
Q7T3M7 PRELIMINARY; PRT; 225 AA.
ID Q7T3M7
AC Q7T3M7
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Death domain-containing tumor necrosis factor receptor superfamily
DE member 23 variant 2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP BRIDGEMAN J.T., JOHNSON A.L.;
RA BRIDGEMAN J.T., JOHNSON A.L.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251408; AAP41834.1; -.
DR HSSP; O14763; IDU3.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR06209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON TER 410 410
SQ SEQUENCE 225 AA; 24697 MW; 59FC9C0AE4530630 CRC64;

Query Match 28.4%; Score 286.5; DB 2; Length 225;
Best Local Similarity 39.6%; Pred. No. 5e-17;
Matches 59; Conservative 26; Mismatches 53; Indels 11; Gaps 5;

Qy 19 RLLLLLLLLLPLQVKFAMLELHSPK-PAGEYWSKDVCKKNSAGTFVKAPCEIPHT 78
Db 4 RAVGLLLLVTLITVP---GSXAEV---CGEYLXEDICMLCPAGTYVAQHCRIHPS 55
Qy 79 QGQCEKCHPG-TTEKDNVLDACILSTCDKQEMVADCSATSDRKCQCRTGLYYYPK 137
Db 56 RKGKASCTEGRDYTAHANGUECLLCRCQKDDQTLTCTVTSTDCQCHQG-YFCPAEG 114
Qy 138 PESCRPCTK-CPOGIPVLQECNSTANTVC 165
Db 115 CEICQRCCTETCPGREGIVQICNATMDLGC 143

RESULT 5
Q7T3M8 PRELIMINARY; PRT; 410 AA.
ID Q7T3M8
AC Q7T3M8
DT 01-OCT-2003 (TrEMBLrel. 25, Created)

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DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Death domain-containing tumor necrosis factor receptor superfamily
DE member 23 variant 1 (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP BRIDGEMAN J.T., JOHNSON A.L.;
RA BRIDGEMAN J.T., JOHNSON A.L.;
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY251408; AAP41833.1; -.
DR HSSP; O14763; IDU3.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Fe4S_ferredoxin.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR06209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4Fe4S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
FT NON TER 410 410
SQ SEQUENCE 410 AA; 46194 MW; 4BFC7C7016C2BA60 CRC64;

Query Match 28.4%; Score 286.5; DB 2; Length 410;
Best Local Similarity 39.6%; Pred. No. 8.7e-17;
Matches 59; Conservative 26; Mismatches 53; Indels 11; Gaps 5;

Qy 19 RLLLLLLLLLPLQVKFAMLELHSPK-PAGEYWSKDVCKKNSAGTFVKAPCEIPHT 78
Db 4 RAVGLLLLVTLITVP---GSXAEV---CGEYLXEDICMLCPAGTYVAQHCRIHPS 55
Qy 79 QGQCEKCHPG-TTEKDNVLDACILSTCDKQEMVADCSATSDRKCQCRTGLYYYPK 137
Db 56 RKGKASCTEGRDYTAHANGUECLLCRCQKDDQTLTCTVTSTDCQCHQG-YFCPAEG 114
Qy 138 PESCRPCTK-CPOGIPVLQECNSTANTVC 165
Db 115 CEICQRCCTETCPGREGIVQICNATMDLGC 143

RESULT 6
Q9DFV0 PRELIMINARY; PRT; 438 AA.
ID Q9DFV0
AC Q9DFV0
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Ovarian TNF receptor.
GN Name=tnfrsf1a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP BRIDGEMAN J.T., JOHNSON A.L.;
RA BOBE J., GOETZ F.W.;
RT "Molecular cloning and expression of a TNF receptor and two TNF
RL ligands in the fish ovary."
RL Comp. Biochem. Physiol. B, Comp. Biochem. 129:475-481 (2001).
DR EMBL; AF250042; AAG24365.1; -.

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DR HSSP; Q92956; LJMA.
DR ZFIN; ZDB-GENE-010802-1; tnfrsf1.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001029; Death.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00150; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 438 AA; 49103 MW; B7E5312BE6B80B04 CRC64;

Query Match 27.3%; Score 275.5; DB 2; Length 438;
Best Local Similarity 39.2%; Pred. No. 8.3e-16;
Matches 49; Conservative 18; Mismatches 51; Indels 7; Gaps 1;

QY 41 LEHSHKCPAGEYMSKDVCKKNSAGTFVKAPCEIHTQGCCKCHPGTFTKDNVLDAC 100
DB 45 LENH-----EYPHNGFCCKNCEAGTYVKEKCTSGHVMGKSPCKEKGTYAEHPTGMEOC 97

QY 101 ILCTCDKQDMVADCSATSDRCKQCTGLYYDPKPPESCRCPTCKPQGIPLVQECNST 160
DB 98 LQSCQCHRDVTVAECTSTNTKCDCKFGTFCFLPDEPCEVCKCTCKADEEVSQCTPT 157

QY 161 ANTVK 165
DB 158 SNTKC 162

RESULT 7
ID Q800K8 PRELIMINARY; PRT; 395 AA.
AC Q800K8;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tumor necrosis factor receptor-1.
GN Name=TNFR-1;
OS Paralicthys olivaceus (Japanese flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Pleuronectoidei; Paralicthyidae; Paralicthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22518447; PubMed=12631519; DOI=10.1016/S0145-305X(02)00118-0;
RA Park C., Kurobe T., Hirano I., Aoki T.;
RT "Cloning and characterization of cDNAs for two distinct tumor necrosis
factor receptor superfamily genes from Japanese flounder Paralicthys
olivaceus."
RL Dev. Comp. Immunol. 27:365-375 (2003).
DR EMBL; AB080946; BAC65225.1; -.
DR HSSP; O14763; 1DU3.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR InterPro; IPR01878; Znf_CCHC.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 2.
DR SMART; SM00208; TNFR; 3.
DR SMART; SM00343; Znf_C2HC; 2.

DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 395 AA; 44304 MW; 8D685A9F74710AE1 CRC64;

Query Match 27.1%; Score 273.5; DB 2; Length 395;
Best Local Similarity 34.1%; Pred. No. 1.1e-15;
Matches 58; Conservative 28; Mismatches 75; Indels 9; Gaps 2;

QY 20 RLILLILLILLNLPL-LQVKFAMLEHSHFKCPAGEYMSKDVCKKNSAGTFVKAPCEIHT 78
DB 9 RLIVLLSSGTVPQSRIDFGRRRTORDILCSNDQNLGNCCNCPAGTHVSHCSKSGE 68

QY 79 QGQCEKCHPGTFTKDNVLDACILCTCDKQDMVADCSATSDRCKQCTGLYYDPKFP 138
DB 69 KGQCCDYRTYTAHPNELNQCFPCRPDPDQIVTFCLTTQDTECCAKAGFCDFPHQAC 128

QY 139 ESCRCPTCKPQGIPLVQECNSTANTVC-----SSSVSRSSASVAWPI 180
DB 129 EVCKCKCKCKEKBEBIRNCTSTNTTECKIKPNKSGSAGNKQVIAVVFPI 178

RESULT 8
ID Q9DF34 PRELIMINARY; PRT; 357 AA.
AC Q9DF34;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Death receptor.
GN Name=hdr;
OS Brachydanio rerio (zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20394298; PubMed=10934476; DOI=10.1038/35019592;
RA Long Q., Huang H., Shafizadeh E., Liu N., Lin S.;
RT "Stimulation of erythropoiesis by inhibiting a new hematopoietic death
receptor in transgenic zebrafish."
RL Nat. Cell Biol. 2:549-552 (2000).
DR EMBL; AF302789; AAG21396.1; -.
DR HSSP; Q92956; LJMA.
DR ZFIN; ZDB-GENE-030826-5; hdr.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_C6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 357 AA; 40662 MW; 1652B4840D9EDBA CRC64;

Query Match 25.7%; Score 259; DB 2; Length 357;
Best Local Similarity 32.9%; Pred. No. 1.8e-14;
Matches 56; Conservative 28; Mismatches 70; Indels 16; Gaps 3;

QY 20 RLILLILLILLNL-----PLQVKFAMLEHSHFKCPAG-FYMSKDVCKKNSA 65
DB 2 RYITLLVLLLVINARSHGDLAWAHSVKNL--SRDVSRCREGLYPHENICCLNCPA 59

QY 66 GTFVKAPCEIHTQGCCKCHPGTFTKDNVLDACILCTCDKQDMVADCSATSDRCKQ 125
DB 60 GTYVKKACAAAABKGVCAPCPFDTYTHDHLGLLKICISCDKCRIDQETIEKTSTQNTRECK 119
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QGLZ4 PRELIMINARY; PRT; 328 AA.  
QGLZ4;  
05-JUL-2004 (TrEMBLrel. 27, Created)  
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
XDR-M1 protein.  
GN Name=XDR-M1;  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Igoellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skaleka U., Smallos D.E., Schnerch A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences".  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.;  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT initiative".  
RL Dev. Dyn. 225:384-391 (2002).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Klein S., Strausberg R.;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC074299; AAH74299.1; -;  
DR GO; GO:0005515; P:protein binding; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0007165; P:signal transduction; IEA.  
DR InterPro; IPR001450; 4Fe4S\_ferredoxin.  
DR InterPro; IPR000488; Death.  
DR InterPro; IPR011029; DEATH like.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00531; Death; 1.  
DR Pfam; PF00020; TNFR\_c6; 1.  
DR SMART; SM00005; DEATH; 1.  
DR SMART; SM00208; TNFR; 3.  
DR PROSITE; PS00198; 4FE4S\_FERREDOXIN; UNKNOWN\_1.  
DR PROSITE; PS50017; DEATH\_DOMAIN; 1.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
SQ SEQUENCE 328 AA; 37262 MW; 7938B5F56F9C5E7 CRC64;  
Query Match 24.6%; Score 248; DB 2; Length 328;  
Best Local Similarity 38.3%; Pred. No. 1.5e-13;  
Matches 49; Conservative 22; Mismatches 55; Indels 2; Gaps 2;  
53 YWSKDVCKKNSAGTFVKAPCEIPHTQOCCKHPG-TFTEKNDYLDACILCTCDKQCE 111

Db 38 YQGNIRCLRCAGTIVBECTTRDTKGCIPCHPGSTYSEGFTGLDCLSCRCRDDQE 97  
QY 112 MVADCSATSDRKQCCKRTGLYYDPKPEPCRPCTK-CPOGIPVLQBCNSTANTVCSSSVS 170  
Db 98 EVRPCTATQNAECRCCKKGYCPMDHPCVCLCTCTESCPCQQLHLPCNSTSDSHCGPAES 157  
QY 171 RRSASVAV 178  
Db 158 GSKLTWIV 165  
RESULT 12  
Q678B7 PRELIMINARY; PRT; 289 AA.  
AC Q678B7;  
DT 25-OCT-2004 (TrEMBLrel. 28, Created)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)  
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
DE Hypothetical protein.  
OS Lymphocystis disease virus - isolate China.  
OC Viruses; dsDNA viruses, no RNA stage; Iridoviridae; Lymphocystivirus.  
OX NCBI\_TaxID=256729;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX PubMed=15194775; DOI=10.1128/JVI.78.13.6982-6994.2004;  
RA Zhang Q.Y., Xiao F., Xie J., Li Z.Q., Gui J.F.;  
RT "Complete Genome Sequence of Lymphocystis Disease Virus Isolated from  
RT China.";  
RL J. Virol. 78:6982-6994 (2004).  
DR EMBL; AY380826; AAU10940.1; -;  
DR InterPro; IPR006209; EGF\_Like.  
DR DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 2.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS01186; EGF\_2; 2.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_2.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
KW Hypothetical protein.  
SQ SEQUENCE 289 AA; 32691 MW; 26B6114D4D5D6C3F CRC64;  
Query Match 23.8%; Score 239.5; DB 2; Length 289;  
Best Local Similarity 38.7%; Pred. No. 7.4e-13;  
Matches 55; Conservative 13; Mismatches 49; Indels 25; Gaps 5;  
QY 24 LLLLLLNLPLQVKFAMLELHSPKAGEYWSKDVCKKNSAGTFVKAPCEIPHTQOCCE 83  
Db 1 MMLFILELPIVHTAT-----DCPPGYISKVY-----PAGT-----PMCS 37  
QY 84 KCHPGTFTEKNDYLDACILCTCDKQCEMVADCSATSDRKQCCKRTGLYYDPKPEPCRP 143  
Db 38 PCSPGTVTGLQNSLRKCLRCSTGSHNEPKVACSTTSDVQCCKRQG-YYVDPE-SEMCFF 95  
QY 144 CTKCPQGPVLPQBCNSTANTVVC 165  
Db 96 CSNCSKSKVKTTCNRTHDTVC 117  
RESULT 13  
Q95185 PRELIMINARY; PRT; 189 AA.  
AC Q95185;  
DT 01-FEB-1997 (TrEMBLrel. 02, Created)  
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Tumour necrosis factor receptor p60 (Fragment).  
GN Name=TNFR-1;  
OS Felis silvestris catus (Cat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
OX NCBI\_TaxID=9685;  
RN [1]  
RP SEQUENCE FROM N.A.



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RA Duthie S., Nasir L., Eckersall P.D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; U72344; AAB95089.1; -.
DR HSSP; P19438; 1EXT.
DR GO; GO:0004872; F:receptor activity; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON TER 189 189
SQ SEQUENCE 189 AA; 21420 MW; F3FBE0CB809D7DBE CRC64;

Query Match 23.7%; Score 239; DB 2; Length 189;
Best Local Similarity 35.3%; Pred. No. 5.5e-13;
Matches 55; Conservative 19; Mismatches 70; Indels 12; Gaps 5;

Qy 22 LLLLLLLLLLPLOVKFAM-----LELHSPKCPAGEY---WSKDVCCNCSAGTFVKAPC 73
Db 13 LVLLALLVEIYPLRVTLGLVPHLRDRKRAIPCPQGGKIHPQDINSICCTCKHKGTYLYNDC 72
Qy 74 EIPHTQGCCKCHPGTFTKDNLYDACILGSTCDKD--QEMVADCSATSRKCCOCTRGLY 131
Db 73 EGPGLDTRCRECGTFTASENLYLRQCLSCSKCKEMYQVEISPTVYRDVTCGRKNQY 132
Qy 132 -YDPKFPESCRCPTKCPQIGIPVLQECNSTANTVCS 166
Db 133 RYVSETHFOCLNGLSLCLNG-TVQISCKETQNTVCT 167

RESULT 14
Q95ND3 PRELIMINARY; PRT; 446 AA.
AC Q95ND3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE Tumor necrosis factor type I.
GN Name=TNFR I;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21425403; PubMed=11531421; DOI=10.1006/viro.2001.1042;
RA Mizuno T., Goto Y., Baba K., Masuda K., Ohno K., Tsujimoto H.;
RT "TNF-alpha-induced cell death in feline immunodeficiency virus-
infected cells is mediated by the caspase cascade.";
RL Virology 287:446-455(2001).
DR EMBL; AB051103; BAB55455.1; -.
DR HSSP; P19438; 1ICH.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR000488; Death.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR006209; EGF like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN_1.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.

Qy 22 LLLLLLLLLLPLOVKFAM-----LELHSPKCPAGEY---WSKDVCCNCSAGTFVKAPC 73
Db 13 LVLLALLVEIYPLRVTLGLVPHLRDRKRAIPCPQGGKIHPQDINSICCTCKHKGTYLYNDC 72
Qy 74 EIPHTQGCCKCHPGTFTKDNLYDACILGSTCDKD--QEMVADCSATSRKCCOCTRGLY 131
Db 73 EGPGLDTRCRECGTFTASENLYLRQCLSCSKCKEMYQVEISPTVYRDVTCGRKNQY 132
Qy 132 -YDPKFPESCRCPTKCPQIGIPVLQECNSTANTVCS 166
Db 133 RYVSETHFOCLNGLSLCLNG-TVQISCKETQNTVCT 167

RESULT 15
Q76B98 PRELIMINARY; PRT; 328 AA.
AC Q76B98
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Death receptor-M2.
GN Name=xDR-M2;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=14668340; DOI=10.1074/jbc.M306217200;
RA Tamura K., Noyama T., Ishizawa Y., Takamatsu N., Shiba T., Ito M.;
RT "Xenopus death receptor-M1 and -M2, new members of the tumor necrosis
factor receptor superfamily, trigger apoptotic signaling by
differential mechanisms.";
RL J. Biol. Chem. 279:7629-7635(2004).
DR EMBL; AB11447; BAD1171.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR001450; 4Pe4s_ferredoxin.
DR InterPro; IPR000488; Death_like.
DR InterPro; IPR011029; DEATH like.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00198; 4PE4S_FERREDOXIN; UNKNOWN_1.
DR PROSITE; PS00017; DEATH DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 328 AA; 36586 MW; 3FCD1CCAB8533355 CRC64;

Query Match 23.0%; Score 232; DB 2; Length 328;
Best Local Similarity 32.7%; Pred. No. 3.7e-12;
Matches 56; Conservative 22; Mismatches 63; Indels 30; Gaps 4;

Qy 2 FGFFCSLVSSLSRWFLRRLLLLLLLLLLLLLNLPLQVKFAMLELHSPKCPAGEYWSKDVCC 61
Db 18 FGFFS-----FLVYSTNGLPLP-----PENYYQAGNTRCL 49
Qy 62 NCSAGTFVKAPCEIPHTQGCCKCHPG-TFTEKDNLYDACILGSTCDKDQEMVADCSATS 120
Db 50 RCPAGTVVGMPCITQDVTGKCFPCHTGSSSEGTGLDHLCLTCLSCRDDQEEVRPCTATQ 109
```



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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: September 8, 2005, 17:05:32 ; Search time 544.286 Seconds  
(without alignments)  
127.905 Million cell updates/sec

Title: us-10-622-407-10

Perfect score: 1008

Sequence: 1 MFGFFCSLVSLSRWFLWRR.....ANTVCSVVSRSSASVAVPI 180

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:\*

- 1: Geneseqp1980s:\*
- 2: Geneseqp1990s:\*
- 3: Geneseqp2000s:\*
- 4: Geneseqp2001s:\*
- 5: Geneseqp2002s:\*
- 6: Geneseqp2003as:\*
- 7: Geneseqp2003bs:\*
- 8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1008	100.0	180	7 ABW02716	Abw02716 Mouse tms
2	1008	100.0	180	8 ADJ45754	Adj45754 Murine tm
3	956	94.8	198	7 ABW02715	Abw02715 Mouse tms
4	956	94.8	198	8 ADJ45752	Adj45752 Murine tm
5	956	94.8	398	7 ABW02717	Abw02717 Mouse tms
6	956	94.8	398	8 ADJ45758	Adj45758 Murine tm
7	748	74.2	133	7 ABW02714	Abw02714 Mouse tms
8	748	74.2	133	8 ADJ45750	Adj45750 Murine tm
9	709	70.3	396	8 ADF57557	Adf57557 Mouse ymk
10	705	69.9	176	2 AAW80254	Aaw80254 Amino aci
11	705	69.9	176	8 ADF57551	Adf57551 Mouse ymk
12	705	69.9	176	8 ADMA46623	Adm46623 Mouse 7F4
13	641	63.6	148	8 ADMA46624	Adm46624 Mouse 7F4
14	542.5	53.8	380	4 ABG09344	Abg09344 Novel hum
15	467	46.3	117	8 ADF57549	Adf57549 Mouse ymk
16	299	29.7	204	5 ABB81467	Abb81467 Murine TA
17	217.5	21.6	247	8 ADF57553	Adf57553 Mouse TNF
18	217.5	21.6	454	5 AAO22289	Aao22289 TNFR1 exp
19	217.5	21.6	454	8 ADT08167	Adt08167 Murine tu
20	208.5	20.7	355	2 AAR85073	Aar85073 Cowpox vi
21	208.5	20.7	355	4 AAB50524	Aab50524 Human tum
22	208.5	20.7	355	8 ADJ96165	Adj96165 Human CRM
23	207.5	20.6	285	2 AAW33359	Aaw33359-TBP (20-19
24	205	20.3	350	5 ABB81468	Abb81468 Viral Crm
25	204.5	20.3	461	7 ADE57927	Ade57927 Rat Prote

26	204.5	20.3	461	8 ADQ76809	Adq76809 Rat solub
27	203.5	20.2	256	2 AAW33357	Aaw33357 TBP (20-16
28	203.5	20.2	307	2 AAW33358	Aaw33358 TBP (20-16
29	203.5	20.2	336	2 AAW33360	Aaw33360 TBP (20-19
30	203.5	20.2	461	2 ABG74754	Abg74754 Rat TNF-R
31	203.5	20.2	461	2 AAR07450	Aar07450 Rat Tumou
32	203.5	20.2	884	2 AAR70109	Aar70109 TNF-R-GBP
33	202.5	20.1	658	5 AAM49759	Aam49759 TNF-selec
34	201.5	20.0	168	2 AAR24084	Aar24084 Truncated
35	201.5	20.0	197	6 ADA49707	Ada49707 Extracell
36	201.5	20.0	199	2 AAR24080	Aar24080 Truncated
37	201.5	20.0	211	2 AAW89225	Aaw89225 Tumour ne
38	201.5	20.0	213	6 ABB95540	Abb95540 Amino aci
39	201.5	20.0	219	8 ADR90159	Adr90159 Human tum
40	201.5	20.0	240	8 ADR90162	Adr90162 Human tum
41	201.5	20.0	247	6 ADA09864	Ada09864 Human rec
42	201.5	20.0	270	8 ADR90160	Adr90160 Human tum
43	201.5	20.0	280	4 AAB66979	Aab66979 Tnf1 pro
44	201.5	20.0	280	8 ADM28817	Adm28817 TNFR supe
45	201.5	20.0	306	8 ADR90161	Adr90161 Human tum

## ALIGNMENTS

## RESULT 1

ABW02716

ID ABW02716 standard; protein; 180 AA.

XX AC ABW02716;

XX DT 11-MAR-2004 (first entry)

XX DE Mouse tmst2-receptor splice variant protein.

XX KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;

XX KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;

XX KW cancer; chromosome identification; gene therapy; antibacterial; virucide;

XX KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;

XX KW cytostatic; mouse; splice variant.

XX OS Mus musculus.

XX PN US6627199-B1.

XX PD 30-SEP-2003.

XX PF 07-JUL-2000; 2000US-00612033.

XX PR 09-JUL-1999; 99US-0143063P.

XX PA (AMGE-) AMGEN INC.

XX PI Saris C;

XX DR WPI; 2003-874309/81.

XX DR N-PSDB; AAD64755.

XX PT New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,

XX PT treating or ameliorating diseases associated with or resulting from

XX PT abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for

XX XX chromosome mapping.

XX PS Claim 1; SEQ ID NO 10; Opp; English.

XX CC The invention relates to transmembrane decoy-receptor (tmst2) proteins

XX CC and their secreted splice variants, belonging to the tumour necrosis

XX CC factor (TNF) receptor super gene family and polynucleotides encoding such

XX CC proteins. The composition and methods are useful in diagnosing, treating

XX CC or ameliorating diseases associated with or resulting from abnormal tmst2

XX CC and/or abnormal expression of its putative ligand, such as sepsis,

XX CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial

XX CC and parasitic diseases or cancer. They may also be used for chromosome

CC identification or mapping. The invention is useful in gene therapy. The  
CC present sequence is mouse tmst2-receptor splice variant protein used in  
CC the exemplification of the invention

AA  
SQ Sequence 180 AA;

	Query Match	100.0%	Score 1008	DB 7	Length 180
	Best Local Similarity	100.0%	Pred. No. 2e-75		
	Matches 180	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	MFGFFCSLVSSLSGRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLELHSPKPAGEYMSKDVC	60		
Db	1	MFGFFCSLVSSLSGRWFLWRRLLLLLLLLLLLLLNLPLQVKFAMLELHSPKPAGEYMSKDVC	60		
Qy	61	KNCAGTFFVKAPCEIPTHQOQCEKCHPGTTEKQNYLDACILCSTCDQOEWADCSATS	120		
Db	61	KNCAGTFFVKAPCEIPTHQOQCEKCHPGTTEKQNYLDACILCSTCDQOEWADCSATS	120		
Qy	121	DRKQCQRTGLYYDDPKPPESCRCPTCKPQGIPLVLOECNSTANTVCCSSSVRRSRASVAWPI	180		
Db	121	DRKQCQRTGLYYDDPKPPESCRCPTCKPQGIPLVLOECNSTANTVCCSSSVRRSRASVAWPI	180		

## RESULT 2

ADJ45754  
ID ADJ45754 standard; protein; 180 AA.

AC ADJ45754;

DT 06-MAY-2004 (first entry)

XX DE Murine tmst2-receptor splice variant polypeptide.

Mouse; tms2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease; cachexia; cancer; cerebral malaria; diabetes mellitus; disseminated intravascular coagulation; haemorrhagic shock; hepatitis; inulin resistance; leprosy; leukaemia; lymphoma; meningitis; multiple sclerosis; ischaemia; obesity; organ rejection; rheumatoid arthritis; septic shock; stroke; adult respiratory distress syndrome; ARDS; tuberculosis; viral disease; tms2-receptor splice variant; receptor.

OS Mus musculus.

XX PN US2004018544-A1.

XX  
PD 29-JAN-2004.

XX  
PF 17-JUL-2003; 2003US-00622407.

XX  
PR 09-JUL-1999: 99US-0143063P.

PR 07-JUL-2000; 2000US-00612033.  
XX

PA (SARI//) SARIS C.  
XX

PI Saris C;  
yy

DR WPI; 2004-224390/21.  
DR N-DEBB. ADT45752.

[illegible]

PT disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial  
PT infections.

XX  
PS  
Claim 13; SEQ ID NO 10; 57pp; English.

xx The invention relates to a tmst2-receptor polypeptides and the  
CC polynucleotide encoding them. The sequences of the invention are useful  
CC for treating diseases and conditions including acquired immunodeficiency  
CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral  
CC malaria, diabetes mellitus, disseminated intravascular coagulation,  
CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,  
CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ

CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory  
CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.  
CC This sequence represents a murine tmst2-receptor splice variant  
CC polypeptide of the invention.

XX Sequence 180 AA; SQ

Query Match	100.0%;	Score 1008;	DB 8;	Length 180;
Best Local Similarity	100.0%;	Pred. No. 2e-75;		
Matches 180;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps 0;				

### RESULT 3

ABW02715  
ID ABW02715 standard; protein; 198 AA.

XX ABW02715;

XX  
DT 11-MAR-2004 (first entry)

XX DE Mouse tmst2-receptor protein.

Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;  
cachexia; autoimmune disease; inflammatory disease; chromosome mapping;  
cancer; chromosome identification; gene therapy; antibacterial; viricide;  
immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;  
cytostatic; mouse.

XX  
OS  
Mus musculus.XX  
PN  
US6627199-B1XX  
PD 30-SEP-2003.XX  
PF 07-JUL-2000: 2000US-00612033.XX  
PR 09-JUL-1999: 99US-0143063P.

XX PA (AMGE-) AMGEN INC.

XX  
PT  
Sarg C:XX  
DB WPT: 2003-874309/81

DR N-PSDB; AAD64754.  
YY

PT New tntst2 nucleic acid molecule and polypeptide, useful for diagnosing  
PT treating or ameliorating diseases associated with or resulting from  
PT abnormal tntst2 expression, e.g. sepsis, inflammation or cancer, or for  
PT chromosome mapping.

XX  
PS Claim 1; SEQ ID NO 8; opp; English.

xx The invention relates to transmembrane decoy-receptor (tmst2) proteins  
cc and their secreted splice variants, belonging to the tumour necrosis  
cc factor (TNF) receptor super gene family and polynucleotides encoding such  
cc proteins. The composition and methods are useful in diagnosing, treating  
cc or ameliorating diseases associated with or resulting from abnormal tmst2  
cc and/or abnormal expression of its putative ligand, such as sepsis,  
cc cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial  
cc and parasitic diseases or cancer. They may also be used for chromosome  
cc identification or mapping. The invention is useful in gene therapy. The

```
CC present sequence is mouse tmst2-receptor protein used in the
CC exemplification of the invention
XX
SQ Sequence 198 AA;

Query Match          94.8%; Score 956; DB 7; Length 198;
Best Local Similarity 100.0%; Pred. No. 4.4e-71;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFFCSLVSSLSRWFLWRRLRLRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
DB 1 MFGFFCSLVSSLSRWFLWRRLRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
QY 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTTEKDNVLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTTEKDNVLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKCQCRGTGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170
DB 121 DRKCQCRGTGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170

RESULT 4
ADJ45752 standard; protein; 198 AA.
XX
AC ADJ45752;
DT 06-MAY-2004 (first entry)
XX
DE Murine tmst2-receptor.
XX
KW Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;
KW autoimmune disease; cachexia; cancer; cerebral malaria;
KW diabetes mellitus; disseminated intravascular coagulation;
KW haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;
KW lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;
KW organ rejection; rheumatoid arthritis; septic shock; stroke;
KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;
KW receptor.
XX
OS Mus musculus.
XX
PN US2004018544-A1.
XX
PD 29-JAN-2004.
XX
PF 17-JUL-2003; 2003US-00622407.
XX
PR 09-JUL-1999; 99US-0143063P.
XX
PR 07-JUL-2000; 2000US-00612033.
XX
PA (SARI/) SARIS C.
XX
PI Saris C;
XX
PI WPI; 2004-224390/21.
XX
DR N-PSDB; ADJ45751.
XX
DR Novel tmst2-receptor polypeptide useful for diagnosing and treating
PT disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial
PT infections.
XX
PS Claim 13; SEQ ID NO 8; 57pp; English.
XX
CC The invention relates to a tmst2-receptor polypeptides and the
CC polynucleotide encoding them. The sequences of the invention are useful
CC for treating diseases and conditions including acquired immunodeficiency
CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral
CC malaria, diabetes mellitus, disseminated intravascular coagulation,
CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,
CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ
CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory
```

```
CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.
CC This sequence represents the murine tmst2-receptor polypeptide of the
CC invention.
XX
SQ Sequence 198 AA;

Query Match          94.8%; Score 956; DB 8; Length 198;
Best Local Similarity 100.0%; Pred. No. 4.4e-71;
Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFGFFCSLVSSLSRWFLWRRLRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
DB 1 MFGFFCSLVSSLSRWFLWRRLRLRLRLRLPLQVKFAMLELHSPKCPAGEYWSKDVC 60
QY 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTTEKDNVLDACILCSTCDKQEMVADCSATS 120
DB 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTTEKDNVLDACILCSTCDKQEMVADCSATS 120
QY 121 DRKCQCRGTGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170
DB 121 DRKCQCRGTGLYYDDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSSVS 170

RESULT 5
ABW02717 standard; protein; 398 AA.
XX
AC ABW02717;
DT 11-MAR-2004 (first entry)
XX
DE Mouse tmst2-receptor-human immunoglobulin Fc region fusion protein.
XX
KW Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;
KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;
KW cancer; chromosome identification; gene therapy; antibacterial; virucide;
KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;
KW cytostatic; mouse; human; immunoglobulin Fc region; fusion protein.
XX
OS Chimeric - Mus musculus.
OS Chimeric - Homo sapiens.
XX
PN US6627199-B1.
XX
PD 30-SEP-2003.
XX
PF 07-JUL-2000; 2000US-00612033.
XX
PR 09-JUL-1999; 99US-0143063P.
XX
PA (AMGE-) AMGEN INC.
XX
PI Saris C;
XX
PI WPI; 2003-874309/81.
XX
DR N-PSDB; AAD64758.
XX
DR New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,
PT treating or ameliorating diseases associated with or resulting from
PT abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for
PT chromosome mapping.
XX
PS Example 4; SEQ ID NO 14; 0pp; English.
XX
CC The invention relates to transmembrane decoy-receptor (tmst2) proteins
CC and their secreted splice variants, belonging to the tumour necrosis
CC factor (TNF) receptor super gene family and polynucleotides encoding such
CC proteins. The composition and methods are useful in diagnosing, treating
CC or ameliorating diseases associated with or resulting from abnormal tmst2
CC and/or abnormal expression of its putative ligand, such as sepsis,
CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial
CC and parasitic diseases or cancer. They may also be used for chromosome
CC identification or mapping. The invention is useful in gene therapy. The
```

CC present sequence is a fusion protein comprising mouse tmst2- receptor  
 CC protein and human immunoglobulin Fc region. This sequence is used in the  
 CC exemplification of the invention

XX SQ Sequence 398 AA;

Query Match 94.8%; Score 956; DB 7; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-71;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTEKDNLYDACILCTCDKQEMVADCSATS 120  
 Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTEKDNLYDACILCTCDKQEMVADCSATS 120  
 Qy 121 DRKQCRRTGLYYDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSVS 170  
 Db 121 DRKQCRRTGLYYDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSVS 170

# RESULT 6

ADJ45758  
 ID ADJ45758 standard; protein; 398 AA.

XX AC ADJ45758;

XX DT 06-MAY-2004 (first entry)

XX DE Murine tmst2-Fc fusion protein.

XX Mouse; tmst2-receptor; acquired immunodeficiency syndrome; AIDS; anaemia;  
 KW autoimmune disease; cachexia; cancer; cerebral malaria;  
 KW diabetes mellitus; disseminated intravascular coagulation;  
 KW haemorrhagic shock; hepatitis; insulin resistance; leprosy; leukaemia;  
 KW lymphoma; meningitis; multiple sclerosis; ischaemia; obesity;  
 KW organ rejection; rheumatoid arthritis; septic shock; stroke;  
 KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;  
 tmst2-Fc fusion protein; receptor.

XX OS Mus musculus.  
 OS Synthetic.

XX FN US2004018544-A1.

XX PD 29-JAN-2004.

XX PF 17-JUL-2003; 2003US-00622407.

XX PR 09-JUL-1999; 99US-0143063P.

XX PR 07-JUL-2000; 2000US-00612033.

XX PA (SARI/) SARIS C.

XX PI Saris C;

XX DR WPI; 2004-224390/21.

XX DR N-PSDB; ADJ45757.

XX Novel tmst2-receptor polypeptide useful for diagnosing and treating  
 PT disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial  
 PT infections.

XX PS Example 4; SEQ ID NO 14; 57pp; English.

XX The invention relates to a tmst2-receptor polypeptides and the  
 CC polynucleotide encoding them. The sequences of the invention are useful  
 CC for treating diseases and conditions including acquired immunodeficiency  
 CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral  
 CC malaria, diabetes mellitus, disseminated intravascular coagulation,  
 CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,

CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ  
 CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory  
 CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.  
 CC This sequence represents a murine tmst2-Fc fusion protein of the  
 CC invention.

XX SQ Sequence 398 AA;

Query Match 94.8%; Score 956; DB 8; Length 398;  
 Best Local Similarity 100.0%; Pred. No. 8.8e-71;  
 Matches 170; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 Qy 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTEKDNLYDACILCTCDKQEMVADCSATS 120  
 Db 61 KNCAGTFVKAPCEIPHTQGCCKCHPGTFTEKDNLYDACILCTCDKQEMVADCSATS 120  
 Qy 121 DRKQCRRTGLYYDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSVS 170  
 Db 121 DRKQCRRTGLYYDPKFPESCRCPTKCPQGIPLVQECNSTANTVCSSVS 170

# RESULT 7

ABW02714

ID ABW02714 standard; protein; 133 AA.

XX AC ABW02714;

XX DT 11-MAR-2004 (first entry)

XX Mouse tmst2-receptor protein from tmst2-00004-d1 clone.

XX Transmembrane decoy-receptor; tmst2; tumour necrosis factor; TNF; sepsis;  
 KW cachexia; autoimmune disease; inflammatory disease; chromosome mapping;  
 KW cancer; chromosome identification; gene therapy; antibacterial; virucide;  
 KW immunosuppressive; immunomodulator; antiinflammatory; antiparasitic;  
 KW cyostatic; mouse.

XX OS Mus musculus.

XX PN US6627199-B1.

XX PD 30-SEP-2003.

XX PF 07-JUL-2000; 2000US-00612033.

XX PR 09-JUL-1999; 99US-0143063P.

XX PA (AMGE-) AMGEN INC.

XX PI Saris C;

XX DR WPI; 2003-874309/81.

XX DR N-PSDB; AAD64753.

XX New tmst2 nucleic acid molecule and polypeptide, useful for diagnosing,  
 PT treating or ameliorating diseases associated with or resulting from  
 PT abnormal tmst2 expression, e.g. sepsis, inflammation or cancer, or for  
 PT chromosome mapping.

XX PS Example 1; SEQ ID NO 6; Opp; English.

XX The invention relates to transmembrane decoy-receptor (tmst2) proteins  
 CC and their secreted splice variants, belonging to the tumour necrosis  
 CC factor (TNF) receptor super gene family and polynucleotides encoding such  
 CC proteins. The composition and methods are useful in diagnosing, treating  
 CC or ameliorating diseases associated with or resulting from abnormal tmst2  
 CC and/or abnormal expression of its putative ligand, such as sepsis,  
 CC cachexia, autoimmune diseases, inflammatory diseases, viral, bacterial  
 CC and parasitic diseases or cancer. They may also be used for chromosome



CC identification or mapping. The invention is useful in gene therapy. The  
 CC present sequence is mouse tmst2-receptor protein used in the  
 CC exemplification of the invention  
 XX  
 SQ Sequence 133 AA;

Query Match 74.2%; Score 748; DB 7; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-54;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 Qy 61 KNCAGTFVVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMWADCSATS 120  
 Db 61 KNCAGTFVVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMWADCSATS 120  
 Qy 121 DRKQCRTGLYYY 133  
 Db 121 DRKQCRTGLYYY 133

RESULT 8  
 ADJ45750  
 ID ADJ45750 standard; protein; 133 AA.  
 XX  
 AC ADJ45750;  
 DT 06-MAY-2004 (first entry)  
 DE  
 XX Murine tmst2 00004-d1 polypeptide.  
 XX Mouse; tmst2-receptor; tmst2 00004-d1;  
 KW acquired immunodeficiency syndrome; AIDS; anaemia; autoimmune disease;  
 KW cachexia; cancer; cerebral malaria; diabetes mellitus; shock; hepatitis;  
 KW disseminated intravascular coagulation; haemorrhagic shock; hepatitis;  
 KW insulin resistance; leprosy; leukaemia; lymphoma; meningitis;  
 KW multiple sclerosis; ischaemia; obesity; organ rejection;  
 KW rheumatoid arthritis; septic shock; stroke;  
 KW adult respiratory distress syndrome; ARDS; tuberculosis; viral disease;  
 KW receptor.  
 XX  
 OS Mus musculus.  
 XX  
 PN US2004018544-A1.  
 XX  
 PD 29-JAN-2004.  
 XX  
 PF 17-JUL-2003; 2003US-00622407.  
 XX  
 PR 09-JUL-1999; 99US-0143063P.  
 PR 07-JUL-2000; 2000US-00612033.  
 XX  
 PA (SARI/) SARIS C.  
 XX  
 PI Saris C;  
 XX  
 DR WPI; 2004-224390/21.  
 DR N-PSDB; ADJ45749.  
 XX  
 PT Novel tmst2-receptor polypeptide useful for diagnosing and treating  
 PT disease e.g., autoimmune disease, cachexia, cancer or viral, bacterial  
 PT infections.  
 XX  
 PS Example 1; SEQ ID NO 6; 57pp; English.  
 XX  
 CC The invention relates to a tmst2-receptor polypeptides and the  
 CC polynucleotide encoding them. The sequences of the invention are useful  
 CC for treating diseases and conditions including acquired immunodeficiency  
 CC syndrome (AIDS), anaemia, autoimmune diseases, cachexia, cancer, cerebral  
 CC malaria, diabetes mellitus, disseminated intravascular coagulation,  
 CC haemorrhagic shock, hepatitis, insulin resistance, leprosy, leukaemia,

CC lymphoma, meningitis, multiple sclerosis, ischaemia, obesity, organ  
 CC rejection, rheumatoid arthritis, septic shock, stroke, adult respiratory  
 CC distress syndrome (ARDS), tuberculosis and a number of viral diseases.  
 CC This sequence represents a murine tmst2-receptor polypeptide clone of the  
 CC invention.  
 XX  
 SQ Sequence 133 AA;

Query Match 74.2%; Score 748; DB 8; Length 133;  
 Best Local Similarity 100.0%; Pred. No. 4.4e-54;  
 Matches 133; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 Db 1 MFGFFCSLVSSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVC 60  
 Qy 61 KNCAGTFVVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMWADCSATS 120  
 Db 61 KNCAGTFVVKAPCEIPHTQGCCKCHPGTFTKDNLDACILCSTCDKQEMWADCSATS 120  
 Qy 121 DRKQCRTGLYYY 133  
 Db 121 DRKQCRTGLYYY 133

RESULT 9  
 ADF57557  
 ID ADF57557 standard; protein; 396 AA.  
 XX  
 AC ADF57557;  
 DT 12-FEB-2004 (first entry)  
 DE  
 XX Mouse ymkz5-human Fc fusion protein.  
 XX Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour;  
 KW cancer; acquired immune deficiency syndrome; AIDS; anaemia;  
 KW autoimmune disease; cachexia; leprosy; leukaemia; hepatitis;  
 KW multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;  
 KW receptor; human.  
 XX  
 OS Chimeric.  
 OS Mus musculus.  
 OS Homo sapiens.  
 XX  
 PN US2003096355-A1.  
 XX  
 PD 22-MAY-2003.  
 XX  
 PF 11-JUL-2002; 2002US-00193616.  
 XX  
 PR 09-JUL-1999; 99US-0143137P.  
 PR 07-JUL-2000; 2000US-00611989.  
 XX  
 PA (ZHAN/) ZHANG K.  
 XX  
 PI Zhang K;  
 XX  
 DR WPI; 2004-008943/01.  
 XX  
 PT Novel ymkz5-receptor polypeptide useful for treating diseases such as  
 PT tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy,  
 PT leukemia, hepatitis, multiple sclerosis.  
 XX  
 PS Example 4; SEQ ID NO 14; 57pp; English.  
 XX  
 CC The invention relates to transmembrane decoy receptor, ymkz5 belonging to  
 CC tumour necrosis factor (TNF) receptor supergene family and nucleic acid  
 CC sequences encoding such receptors. The invention is useful for detecting  
 CC diseases or susceptibility to diseases related to the presence of mutated  
 CC ymkz5-receptor gene such as tumours or cancers. The sequences of the  
 CC invention are used as medication for a number of diseases such as  
 CC acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases,

CC cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial  
CC ischaemia, obesity etc. The invention is also useful in gene therapy. The  
CC present sequence is mouse ymkz5-human fc fusion protein.

SQ Sequence 396 AA;

Query Match 70.3%; Score 709; DB 8; Length 396;  
Best Local Similarity 78.6%; Pred. No. 2.2e-50;  
Matches 132; Conservative 6; Mismatches 22; Indels 8; Gaps 1;

QY 7 SLVSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCAG 66

Db 5 SHVSSLSHWF-----LLLLLLLLLPLVIFAMPESYSFNCPPGEYQSDVCCCKTCPSG 56

QY 67 TFVKAPCEIPHTQGCCKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATSDRKCQC 126

Db 57 TFVKAPCKIPHTQGCCKCHPGTFTKDNGLHDCCLCSTCDKQNMVADCSATSDRKCCEC 116

QY 127 RTGLYYDDPKPEPESCRCTKCPQGIPLVQECNSTANTVCSSVSRRSA 174

Db 117 QIGLYYYDDPKPEPESCRCTKCPQGIPLVQECNSTANTVCSSVSNAAA 164

RESULT 10

AAW80254  
ID AAW80254 standard; protein; 176 AA.

XX AC AAW80254;

XX DT 28-JAN-1999 (first entry)

XX DE Amino acid sequence of protein 7F4.

XX KW Protein 7F4; differentiation; osteoblast cell; bone growth; bone sarcoma.

XX OS Unidentified.

XX FH Key Location/Qualifiers  
XX FT Peptide 1..28

XX FT /note= "signal peptide"

XX FT Protein 29..176

XX FT /note= "mature protein"

XX FN WO9843998-A1.

XX PD 08-OCT-1998.

XX PF 01-APR-1998; 98WO-JP001511.

XX PR 01-APR-1997; 97JP-00099653.

XX PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.

XX PI Kimura N, Toyoshima T;

XX WPI; 1998-568275/48.

XX DR N-PSDB; AAV68046.

XX PT Receptor protein inducing differentiation in osteoblast cells - has  
XX PT extracellular region only and can be used for screening substances for  
XX PT treatment of bone growth disorders.

XX PS Claim 1; Page 29-31; Sipp; Japanese.

XX CC The present sequence represents a protein designated 7F4. This protein is  
XX CC capable of inducing differentiation in osteoblast cells. The protein may  
XX CC be used to screen compounds for the ability to bind to it, for use as  
XX CC ligands, agonists or antagonists and inhibiting or otherwise altering its  
XX CC differentiation inducing activity. Compounds so identified, as well as  
XX CC the protein itself, DNA encoding it, and antibodies to it, may be used in  
XX CC the treatment of diseases of bone growth and osteoblast differentiation,  
XX CC such as bone sarcomas

SQ Sequence 176 AA;

Query Match 69.9%; Score 705; DB 2; Length 176;  
Best Local Similarity 79.9%; Pred. No. 2.1e-50;  
Matches 131; Conservative 5; Mismatches 20; Indels 8; Gaps 1;

QY 7 SLVSLSRWFLWRRLLLLLLLLLLLLLPLQVKFAMLELHSPKCPAGEYWSKDVCCKNCAG 66

Db 5 SHVSSLSHWF-----LLLLLLLLLPLVIFAMPESYSFNCPPGEYQSDVCCCKTCPSG 56

QY 67 TFVKAPCEIPHTQGCCKCHPGTFTKDNLYLDACILCSTCDKQEMVADCSATSDRKCQC 126

Db 57 TFVKAPCKIPHTQGCCKCHPGTFTKDNGLHDCCLCSTCDKQNMVADCSATSDRKCCEC 116

QY 127 RTGLYYDDPKPEPESCRCTKCPQGIPLVQECNSTANTVCSSVS 170

Db 117 QIGLYYYDDPKPEPESCRCTKCPQGIPLVQECNSTANTVCSSVS 160

RESULT 11

ADF57551

ID ADF57551 standard; protein; 176 AA.

XX AC ADF57551;

XX DT 12-FEB-2004 (first entry)

XX DE Mouse ymkz5 receptor.

XX KW Transmembrane decoy receptor; ymkz5; tumour necrosis factor; TNF; tumour;  
XX KW cancer; acquired immune deficiency syndrome; AIDS; anaemia;  
XX KW autoimmune disease; cachexia; leprosy; leukaemia; hepatitis;  
XX KW multiple sclerosis; myocardial ischaemia; obesity; gene therapy; mouse;  
XX KW receptor.

XX OS Mus musculus.

XX PN US2003096355-A1.

XX PD 22-MAY-2003.

XX PF 11-JUL-2002; 2002US-00193616.

XX PR 09-JUL-1999; 99US-0143137P.

XX PR 07-JUL-2000; 2000US-00611989.

XX PA (ZHAN/) ZHANG K.

XX PI Zhang K;

XX WPI; 2004-008943/01.

XX DR N-PSDB; ADF57550.

XX PT Novel ymkz5-receptor polypeptide useful for treating diseases such as  
XX PT tumor, cancer, AIDS, anemia, autoimmune diseases, cachexia, leprosy,  
XX PT leukemia, hepatitis, multiple sclerosis.  
XX PS Claim 13; SEQ ID NO 8; 57pp; English.

XX CC The invention relates to transmembrane decoy receptor, ymkz5 belonging to  
XX CC tumour necrosis factor (TNF) receptor supergene family and nucleic acid  
XX CC sequences encoding such receptors. The invention is useful for detecting  
XX CC diseases or susceptibility to diseases related to the presence of mutated  
XX CC ymkz5-receptor gene such as tumours or cancers. The sequences of the  
XX CC invention are used as medication for a number of diseases such as  
XX CC acquired immune deficiency syndrome (AIDS), anaemia, autoimmune diseases,  
XX CC cachexia, leprosy, leukaemia, hepatitis, multiple sclerosis, myocardial  
XX CC ischaemia, obesity etc. The invention is also useful in gene therapy. The  
XX CC present sequence is mouse ymkz5 receptor protein.

SQ Sequence 176 AA;

Query Match 69.9%; Score 705; DB 8; Length 176;

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: |||||
Db 117 QIGLYYDPKPPBSRCPCTKCPQGIPLVQECNSTANTVCSSVS 160
|||||

RESULT 13
ADM46624
ID ADM46624 standard; protein; 148 AA.
XX
XX ADM46624;
XX
XX 17-JUN-2004 (first entry)
XX
XX Mouse 7F4 protein #2.
XX
XX 7F4 gene; Osteopathic; Anorectic; Antidiabetic;
XX glycolipid metabolism disorder; osteoporosis; obesity; di
XX
XX Mus musculus.
XX
XX W02004026026-A1.
XX
XX 01-APR-2004.
XX
XX 10-SEP-2003; 2003WO-JP011545.
XX
XX 17-SEP-2002; 2002JP-00270321.
XX
XX (CHUS ) CHUGAI SEIYAKU KK.
XX
XX Kake T, Saito H, Makishima F;
XX
XX WPI; 2004-340227/31.
XX
XX Transgenic non-human animal with modified expression of 7
XX screening remedies for bone or glycolipid metabolism diso
XX
XX Claim 3; SEQ ID NO 3; 44pp; Japanese.
XX
XX The present invention relates to a transgenic non-human a
XX expression of 7F4 gene artificially modified. The transge
XX a disease model for bone and glycolipid metabolism disor
XX identified by the screening method are agents for the pre
XX treatment of diseases including osteoporosis, obesity and
XX present sequence represents the modified mouse 7F4 protei
XX
XX Sequence 148 AA;
XX
XX Query Match 63.6%; Score 641; DB 8; Length 14
XX Best Local Similarity 84.8%; Pred. NO. 3.3e-45;
XX Matches 112; Conservative 5; Mismatches 15; Indels
XX
XX 39 AMLELHFKPAGBYWSKDVCKNCSAGTFVKAPCEIPHTQGQCEKCH
XX
XX 1 AMPEYSYFNCPDEGYQSNVCKTCTPSGTFVKAPCKIPHTQGQCEKCH
XX
XX 99 ACILCSTCDKQEMVADCSATSDRKQCRCRTGLYYDPKFPESCRCPTK
XX
XX 61 DCELCSTCDKQNMVADCSATSDRKCECQIGLYYDPKFPESCRCPTK
XX
XX 159 STANTVCSSVS 170
XX
XX 121 STANTVCSSVS 132
XX

RESULT 14
ABG09344
ID ABG09344 standard; protein; 380 AA.
XX
XX ABG09344;
XX
XX 13-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #9335.

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